

GenCore version 4.5  
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OK protein - protein search, using sw model

Run on: October 12, 2001, 16:09:03 ; Search time 22.7 Seconds  
(without alignments)  
1812.637 Million cell updates/sec

Title: US-09-265-540E-2  
Perfect score: 1627  
Sequence: 1 MQFTWLEIEITSLFMWF.....VDACATAVMSPEELLRAWIS 311

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues  
Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: SPTRMBL\_16:\*  
2: sp\_archaea:\*  
3: sp\_bacteria:\*  
4: sp\_fungi:\*  
5: sp\_human:\*  
6: sp\_invertebrate:\*  
7: sp\_mammal:\*  
8: sp\_mmc:\*  
9: sp\_organellae:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_unclassified:\*  
13: sp\_vertebrate:\*  
14: sp\_virus:\*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	202	12.4	569	13	O9YHWO_gallus gall
2	171.5	10.5	442	13	O9PVW9
3	166.5	10.2	341	13	O9YGC8
4	157	9.6	332	11	O63953
5	153.5	9.4	308	13	O9PVK0
6	150.5	9.3	508	13	O9YHV9
7	138	8.5	553	4	O9UHF4
8	115	7.1	298	4	O9HD97
9	113	6.9	301	4	O95100
10	110.5	6.8	299	4	O9UBK4
11	108.5	6.7	299	4	O9UGN4
12	105.5	6.5	332	6	O9GK86
13	101.5	6.2	509	6	O9MYZ9
14	100.5	6.2	419	10	O9M0H3
15	98.5	6.1	484	4	O14936
16	97.5	6.0	229	6	O27950
17	95.5	5.9	229	6	O28206
18	95.5	5.9	1427	13	O91562
19	95	5.8	1445	11	O63155

20	92.5	5.7	666	13	O73876	O73876 brachydanio
21	92.5	5.7	1118	4	O15426	O15426 homo sapien
22	92	5.7	422	4	O9UHH5	O9UHH5 homo sapien
23	91.5	5.6	987	13	O73875	O73875 brachydanio
24	91.5	5.6	1115	4	O9HD43	O9HD43 homo sapien
25	91	5.6	422	4	O75462	O75462 homo sapien
26	91	5.6	425	11	O9JMS8	O9JMS8 mus musculu
27	88	5.4	1527	11	O9E67	O9E67 rattus norv
28	87.5	5.4	227	8	O9G3S0	O9G3S0 challoolobu
29	87.5	5.4	1274	3	O9UN05	O9UN05 schizosach
30	87	5.3	896	11	O64146	O64146 rattus norv
31	86	5.3	227	8	O37596	O37596 phyllotomu
32	86	5.3	227	8	O9G390	O9G390 echinops te
33	86	5.3	228	8	O9ML06	O9ML06 limulus pol
34	86	5.3	495	2	O34660	O34660 bacillus su
35	85.5	5.3	1647	5	O9YVW1	O9YVW1 dtrosophila
36	85	5.2	227	8	O9G947	O9G947 propithecus
37	85	5.2	592	4	O95697	O95697 homo sapien
38	85	5.2	1294	4	O9UQP3	O9UQP3 homo sapien
39	84.5	5.2	345	5	P91030	P91030 caenorhabdi
40	84.5	5.2	752	1	O9YCG1	O9YCG1 aeropyrum p
41	84.5	5.2	1252	11	O9E0S9	O9E0S9 mus musculu
42	84	5.2	227	8	O9MET3	O9MET3 pysester ca
43	84	5.2	227	8	O9G6N2	O9G6N2 pteropus da
44	84	5.2	2297	3	O9HGK6	O9HGK6 candida alb
45	83.5	5.1	220	8	O9XN00	O9XN00 stomaphis a

## ALIGNMENTS

RESULT	1	PRELIMINARY:	PRT:	569 AA.
O9YHWO				
ID	O9YHWO			
AC	O9YHWO			
DT	01-MAY-1999 (TREMBLrel. 10, Created)			
DT	01-MAY-1999 (TREMBLrel. 10, Last sequence update)			
DE	01-MAR-2001 (TREMBLrel. 16, Last annotation update)			
DE	INTERFERON ALPHA/BETA RECEPTOR 1.			
GN	IFNARI.			
OS	Gallus gallus (Chicken).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;			
OC	Gallus.			
OX	NCBI_TaxID=9031.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=LIVER;			
RA	Reboul J., Gardiner K., Monneron D., Uze G., Lutfalla G.;			
RT	*Comparative genomic analysis of the Interferon/Interleukin-10			
RT	receptor gene cluster.";			
RL	Genome Res. 0:0-0(1999).			
DR	EMBL: AF082664; AADI369.1; -.			
DR	InterPro: IPR000282; -.			
DR	InterPro: IPR001777; -.			
DR	pfam: PF00041; fn3; 1.			
KW	SMART: SM00060; FN3; 1.			
RECEPTOR.				
SQ	SEQUENCE 569 AA; 64055 MW; 6A757DDEFB91E605 CRC64;			

Query Match	12.4%;	Score 202;	DB 13;	Length 569;
Best Local Similarity	25.2%;	Pred. No. 1.1e-10;		
Matches 79;	Conservative 50;	Mismatches 127;	Indels 58;	Gaps 14;
OY	21 YALIPCL-LTDEVALPAPONLSVLTNMKLLMWSFVIAAGETVYVSVEY-OGEYESLY 78			
DB	222 FSDIHCKITRKVNDLCPINVRFAALNMKFYLLMDNHY--NEHVYTVQVLTITKLY 279			
OY	79 T--SHIWPSSWCSLTGEPEDVTDITAT-VPIYLNVRATIGSOTSAMS----- 125			
DB	280 DDVSSKNQKVSCEINTSMKCNLSIVIKPTISASYFRVQAMNEXSKCLSDVEVDPPVT 339			

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QY 126 -----ILKHPNRNSTILTRPGMEIKKXGFHVLIELEDGPOFEFLVAYWX 171
DB 340 NEIGPPPVKVDISDYLH-----IKITPG-----GPGNKIMSDLYD----FSYQILYWK 385
QY 172 REPGAEEHVKMNNSGGIPVHLETPGAAVCVKAQTFVKAIGXYSASFQECV- EVGGEA 230
DB 386 NSSDNEEVKMKETKQIATVSDIAPSTLCVKQAFSEAVKNSDSFRECICIGAGKH 445
QY 231 IPLVLAFAVGFLLIIVVP-----LFWMKGRLLQYSCCPVVVLPDTL-----KITNSP 281
DB 446 LPLIT-LATFGALTVLVLIASLVIFFLQYVKNIKYMFPSQTPLEIIEGFGALFSSP 504
QY 282 OKLISCRREVDAC 295
DB 505 --FVPTVEEPVEIC 516

RESULT 2
Q9PVJ9 PRELIMINARY: PRT: 442 AA.
Q9PVJ9
01-MAY-2000 (Tremblrel. 13, Created)
01-MAY-2000 (Tremblrel. 13, Last sequence update)
01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE INTERFERON ALPHA/BETA RECEPTOR 1 (FRAGMENT).
GN IFNARI.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
NCBI_TaxID=9031;
RN [1]
RX MEDLINE=99177346; PubMed=10077530;
RA Reboul J., Gardiner K., Monneron D., Uze G., Lutfalla G.;
*Comparative genomic analysis of the Interferon/Interleukin-10
RT receptor gene cluster.
RL Genome Res. 9:242-250(1999).
DR EMBL: AF082667; AAD13679.1; -.
DR InterPro: IPR001777; -.
DR InterPro: IPR001777; -.
DR Pfam: PF00041; fn3; 1.
DR SMART: SM00060; FN3; 1.
KW Receptor.
FT NON-TER
SQ SEQUENCE 442 AA; 49877 MW; 839EBE92170609E0 CRC64;

Query Match 10.5%; Score 171.5; DB 13; Length 442;
Best Local Similarity 27.0%; Pred. No. 5.8e-08;
Matches 64; Conservative 29; Mismatches 99; Indels 45; Gaps 9;

QY 21 YALPCL-LTDEVALTPAPONLSVSTNMKHLMMSPYIAPGEVYVSVEY-OGESYSLY 78
DB 222 FSPFHCKTKTRKVDLCLPTVRFALNMKRYLLMDNHY--NEHYTTVOVLITGLKMLY 279
QY 79 T--SHIWPSSWCSLTGEGPCDVTDDITAT--VPYNLRVRAIGSOTSAMS----- 125
DB 280 DDYSKMKQKSGCENITSMKCNLSVYIKPTSASYFRVQANNEYKNSCLSKDVEVDPEVT 339
QY 126 -----ILKHPNRNSTILTRPGMEIKKXGFHVLIELEDGPOFEFLVAYWX 171
DB 340 NEIGPPPVKVDISDYLH-----IKITPG-----GPGNKIMSDLYD----FSYQILYWK 385
QY 172 REPGAEEHVKMNNSGGIPVHLETPGAAVCVKAQTFVKAIGXYSASFQECV- EVGGEA 230
DB 386 NSSDNEEVKMKETKQIATVSDIAPSTLCVKQAFSEAVKNSDSFRECICIGAGKH 445

RESULT 3
Q9YGC8 PRELIMINARY: PRT: 341 AA.
AC Q9YGC8;
Q9YGC8;
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DT 01-MAY-1999 (Tremblrel. 10, Created)
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE INTERLEUKIN-10 RECEPTOR 2.
GN IL10R2.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
NCBI_TaxID=9031;
RN [1]
RX MEDLINE=94170381; PubMed=8124717;
RA Hemmi S., Bohni R., Stark G., Di Marco F., Aguet M.;
*A novel member of the interferon receptor family complements
RT functionality of the murine interferon gamma receptor in human

QY 22 ALPCLTDEVALTPAPONLSVSTNMKHLMMSPYIAPGEVYVSVEY-OGESYSLY 81
DB 8 ALMGLLCLVSGSIVPRKPNARISVNFBSVLLMDPGVKNISTVQ-----AKS 58
QY 82 IWPSSWCSLTGEGPCDVTDDITATVPYNLRVRAIGSOTSAMSILKHPNRNSTIL 138
DB 59 IFPKQNFNNVTNLNLTVECDVS-SLSVYGAIVLRVTEMEDEHSDMAVYRFK-PMADTVI 116
QY 139 TRPGMEIKKXGFHVLIELEDGPOFE-----FLVAYKREPGAEEHVK 182
DB 117 GPPSVNVKSESGLTHVDF--TGPAADREHDKWSLKQYGSWYRILYMKK--GSNKKV-- 170
QY 183 VASGIGPHELT-----MEPGAAYCVKAQTFVKAIGXYSASFQECV-OGESYSLY 232
DB 171 -----IHIDKHNSEILSLEPWTITICIQYQGVIPENMKTGERSQELCEQTTNGVTP 223
QY 233 LVLAFAVGFML-ILVVVPL--FVWMKGRLLQYSCCPVVVLPDTLKITNSP 281
DB 224 WIVVTVLLGSLMAVIISVPCFFAFWLYLRFTHVFPFSYIFPOLKREFFSP 276

RESULT 4
Q63953 PRELIMINARY: PRT: 332 AA.
AC Q63953;
Q63953
01-NOV-1996 (Tremblrel. 01, Created)
01-NOV-1996 (Tremblrel. 01, Last sequence update)
01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE INTERFERON GAMMA RECEPTOR 2 (INTERFERON GAMMA RECEPTOR BETA SUBUNIT).
GN IFNGR2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RX MEDLINE=94170381; PubMed=8124717;
RA Hemmi S., Bohni R., Stark G., Di Marco F., Aguet M.;
*A novel member of the murine interferon gamma receptor in human
RT functionality of the murine interferon gamma receptor in human
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RT cells."
RL Cell 76:803-810(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=128SV/7;
RX MEDLINE=97128072; PubMed=8972742;
RA Ebersberger C., Rhee S., Muthukumar G., Lembo D., Donnelly R.,
RA Pestle S., Dambic Z.;
RT "Genomic organization and promoter analysis of the gene ifng2
RT encoding the second chain of the mouse interferon-gamma receptor.";
RL Scand. J. Immunol. 44:599-606(1996).
DR EMBL; U69599; AAC52938.1; JOINED.
DR EMBL; U69594; AAC52938.1; JOINED.
DR EMBL; U69595; AAC52938.1; JOINED.
DR EMBL; U69596; AAC52938.1; JOINED.
DR EMBL; U69597; AAC52938.1; JOINED.
DR EMBL; U69598; AAC52938.1; JOINED.
DR EMBL; S69336; AAB30165.1; JOINED.
DR MGI; MGI:107654; Ifng2.
DR InterPro: IPR000282; -.
DR Pfam: PF00041; fn3; 1.
DR SMART; SM00060; FN3; 1.
SQ SEQUENCE 332 AA; 37471 MW; E2DD53BF934BA087 CRC64;

Query Match 9.6%; Score 157; DB 11; Length 332;
Best Local Similarity 27.0%; Pred. No. 9.5e-07;
Matches 72; Conservative 34; Mismatches 101; Indels 60; Gaps 17;

QY 17 MWFYALIPCLL-----TDEVALIPAPQNLSTNKKHLMSPVIAPEGTVYY 66
DB 6 LW-----LPSLLCGLGAASPSQSLAPLNLRLHLNYDEQILTWEP--SPSNDNR 58
QY 67 SVEYGEESLTSHTWIPSSWCSLTEGPC-DVTD---DITR-----TVPYN--LKY 113
DB 59 PAVYGVES-----FIDGSHWRLLE-PNCTDITETKCDLGGGRLKLPFPFTVFLRY 110
QY 114 RATLSGTSAMSILKHPFNRSITLTPR--GMEIKKXGFHLYTELE---DL--GPOFEFL 166
DB 111 RAKRNLTSKMWGLE-PROHYENVTYGPCKNISVTPGKSLVHSPDPVEHGATFYIL 169
QY 167 VAYMXREPQAEHVK-MVRSGGIPVHLETPMGAAYCVKAQTFV---KAIGYSAFSQT 221
DB 170 VHYWKSSEYQGVQVGPFFNSIV--LGNLKYRYVCLOTEQGLIKNKIRHGLLSNV 227
QY 222 ECVEVQGEA-----IPVLALFAFV 241
DB 228 SCHETTANASARLQGVILPIGLIFALL 254

RESULT 5
ID Q9PVK0 PRELIMINARY; PRT; 508 AA.
AC Q9PVK0;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE INTERFERON ALPHA/BETA RECEPTOR 2.
GN IFNAR2.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=99177346; PubMed=10077530;
RA Reboul J., Gardiner K., Monneron D., Uze G., Lutfalla G.;
RT "Comparative genomic analysis of the interferon/interleukin-10
RT receptor gene cluster.";
RL Genome Res. 9:242-250(1999).
DR EMBL; AF082667; AAD13677.1; -.

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DR HSSP; P24055; 1A21.
DR InterPro: IPR000282; -.
DR InterPro: IPR000342; -.
DR InterPro: IPR001187; -.
DR InterPro: IPR002048; -.
DR Pfam; PF01108; Tissue_fac; 1.
DR PRINTS; PR00346; TISSUEFACTOR.
DR ProDom; PD001580; -.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.
KW Receptor.
SQ SEQUENCE 508 AA; 57175 MW; 4C02D29D243E8C05 CRC64;

Query Match 9.4%; Score 153.5; DB 13; Length 508;
Best Local Similarity 24.7%; Pred. No. 3.4e-06;
Matches 73; Conservative 46; Mismatches 116; Indels 61; Gaps 16;

QY 20 FYALI-----PCL-LTDEVALIPAPQNLSTNKKHLMSPVIAPEGTVYSVEY 70
DB 11 FYQLVFSILCAACYSLSERKPREP-PDNLQMTSNNFQHTLSWRASDPTVPTVRY-- 67
QY 71 QGEYESLTSHTI-WIPSSWCSLTEGPCDVTDDI-TATVPTNLAVKATIGSQTAMSL- 127
DB 68 -----LYSSHSMWKIAKQCSRIYQPCNLTDDQVYVDSFSAFVQSFVTEVNSSILY 121
QY 128 -----KHPFNRSITI-----LTPQMEIKKXGFHLYTELELIGPOFEFLVAYWX 171
DB 122 FSPLSERFLCPERNLSSCHVCHINTITKLPPTHLRKNG--KLSLFDIYNKVNVEIT--L 177
QY 172 REPQAEHVK--MVRSGGIPVHLETPMGAAYCVKAQTFVKAIGXYSASFQTECEVQV 228
DB 178 RTVG-EERKSRSEKVEEPEPSIVELYPNRNCVSVWV-TASLNKHSIPAMKCIITDS 235
QY 229 EA-----IPVLALFAFVGMILVYVPLFVWKMGLLQSCCPVYVLPFLKIT 278
DB 236 VAEKDYGITITAVA---ICFSILVYLKCLHLGTYLHRKS-----LPDTLVET 282

RESULT 6
ID Q9YHV9 PRELIMINARY; PRT; 508 AA.
AC Q9YHV9;
DT 01-MAY-1999 (Tremblrel. 10, Created)
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)
DE INTERFERON ALPHA/BETA RECEPTOR 2.
GN IFNAR2.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Reboul J., Gardiner K., Monneron D., Uze G., Lutfalla G.;
RT "Comparative genomic analysis of the interferon/interleukin-10
RT receptor gene cluster.";
RL Genome Res. 0:0-0(1999).
DR EMBL; AF082665; AAD13670.1; -.
DR HSSP; P24055; 1A21.
DR InterPro: IPR000282; -.
DR InterPro: IPR001187; -.
DR Pfam; PF01108; Tissue_fac; 1.
DR PRINTS; PR00346; TISSUEFACTOR.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.
KW Receptor.
SQ SEQUENCE 508 AA; 57049 MW; 5CE6DFED970DFB90 CRC64;

Query Match 9.3%; Score 150.5; DB 13; Length 508;
Best Local Similarity 24.3%; Pred. No. 6.0e-06;

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OY 251 PLFYKMG 258  
 DB 403 VLEIVTVG 410

Search completed: October 12, 2001, 16:11:08  
 Job time: 125 sec

RESULT 15

ID Q14936 PRELIMINARY; PRT; 484 AA.  
 AC Q14936;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)  
 DT 01-OCT-2000 (TREMBLrel. 15, last annotation update)  
 DE INTERFERON-GAMMA RECEPTOR ALPHA CHAIN.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euthera; Primates; Catarrhini; Homidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=89003065; PubMed=2971451;  
 RX Aguet M., Dembic Z., Merlin G.;  
 "Molecular cloning and expression of the human interferon gamma  
 receptor";  
 RL Cell 55:273-280(1988).  
 RN [2]  
 RP PARTIAL SEQUENCE FROM N.A.  
 RX MEDLINE=97246734; PubMed=9089099;  
 RX Merlin G., van der Leede B.-J.M., McKune K., Knezevic N.,  
 Bannwarth W., Romguin N., Viegas-Requignot E., Kiefer H., Aguet M.,  
 Dembic Z.;  
 "The gene for the ligand binding chain of the human interferon gamma  
 receptor";  
 RL Immunogenetics 45:413-421(1997).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Dembic Z.;  
 RL Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; U19247; AAC52064.1; JOINED.  
 DR EMBL; U19242; AAC52064.1; JOINED.  
 DR EMBL; U19243; AAC52064.1; JOINED.  
 DR EMBL; U19244; AAC52064.1; JOINED.  
 DR EMBL; U19245; AAC52064.1; JOINED.  
 DR EMBL; U19246; AAC52064.1; JOINED.  
 DR HSSP; P15260; JURN.  
 DR InterPro; IPR000282;  
 SO SEQUENCE 484 AA; 53818 MW; 780B59C2B2C24A2C CRC64;

Query Match 6.1%; Score 98.5; DB 4; Length 484;  
 Best Local Similarity 20.8%; Pred. No. 0.5; Mismatches 100; Indels 71; Gaps 14;  
 Matches 59; Conservative 53;

OY 35 LPAPQNLSTNMKHLMSVIAGETVY-----YSVEYQGEYESLYTSHIWIPSSW 88  
 DB 29 VPTPTNVTIESYNNMPTIYWEQIMPOVPTVEYKNGVK-----NSEWIDA-- 76  
 OY 89 CSLTGFPCDVTDDITATVPYN---LVRATIGSOTSAMSIILKHPNRSNSTITLRPMET 145  
 DB 77 CINISHAKCNISDHGD--PSNSLWVRKARVGOESAVAKSEEFVAVCRDGIKIPKIDI 134  
 OY 146 KXGPHLYTEL-----EDLGPQFE-PLVAV--WKREPGAEHVKWVRSG--- 186  
 DB 135 RKEEKQIMIDIFHPSVFVNGDEQVDYDEPTCTIRVINYVNMNGSELTQYKILTOKEDD 194  
 OY 187 -----GIPVHETMEPGAAYCVKAQTFVKAIGXYSAFSQTECEVVOGEA-----IP 232  
 DB 195 CDEICQQLAIPV---SSLNSQYC-SABGVLHWGVTTEKSKVCTITINSSIKSGLWIP 249  
 OY 233 LVLAIFAFAVFMILIVVPLFYKMGRLQYSCCPVVVLPDTL 275  
 DB 250 VVAAL-----VLSLVFICFYIKINPLKES-----IILPKSL 282





GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: October 12, 2001, 16:08:43 ; Search time 16 Seconds  
(without alignments)  
1480.643 Million cell updates/sec

Title: US-09-265-540E-2

Perfect score: 1627  
Sequence: 1 MDTFTVLEIEIWTSLFEMFP.....VDACATVMSPEILLRAMIS 311

Scoring table: BL0SUM62  
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_68:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	191	11.7	325	2 A47003	cytokine receptor
2	178.5	11.0	337	2 I38500	interferon gamma r
3	178.5	11.0	590	2 A45283	interferon alpha/b
4	175.5	10.8	349	2 JC6311	interferon recepto
5	164.5	10.1	560	2 S27387	interferon alpha r
6	162.5	10.0	557	2 A32694	interferon alpha/b
7	157	9.6	332	2 A49947	interferon gamma r
8	136	8.4	578	2 I56215	interleukin-10 rec
9	130	8.0	292	1 KFRB3	tissue factor prec
10	125.5	7.7	295	1 KFRH3	tissue factor prec
11	125.5	7.4	575	2 A49667	tissue factor prec
12	121	7.4	489	2 A31555	interleukin-10 rec
13	116.5	7.2	294	1 KFRM3	tissue factor prec
14	114.5	7.0	292	1 KFRB3	tissue factor prec
15	114	7.0	507	1 A32385	erythropoietin rec
16	100.5	6.2	419	2 T10652	hypothetical prote
17	99	6.1	507	1 A46713	erythropoietin rec
18	97	6.0	508	1 ZOHUR	erythropoietin rec
19	96	5.9	984	2 A39753	protein-tyrosine-p
20	95.5	5.9	1427	2 I51669	tumor suppressor k
21	95	5.8	1447	2 A54100	tumor suppressor p
22	92.5	5.7	987	2 A54092	protein-tyrosine k
23	92.5	5.7	1118	1 A49724	prolactin receptor
24	89	5.5	831	2 J01655	prolactin receptor
25	89	5.5	977	2 S49004	tyrosine kinase Mp
26	88.5	5.4	1928	2 J50610	beta-galactosidase
27	88	5.4	265	2 S14081	erythropoietin rec
28	88	5.4	985	2 I51549	receptor tyrosine
29	87.5	5.4	1274	2 T39249	probable tripeptid

30	87	5.3	896	2 I56563	interleukin-3 rece
31	87	5.3	952	2 I50612	protein-tyrosine k
32	86	5.3	227	2 I37081	cytochrome-c oxida
33	86	5.3	227	2 T11483	cytochrome-c oxida
34	86	5.3	379	2 S56193	probable membrane
35	86	5.3	405	2 H69614	aldehyde dehydroge
36	85.5	5.3	1557	2 D41214	protein-tyrosine-p
37	85.5	5.3	1630	2 C41214	protein-tyrosine-p
38	85	5.2	227	2 T11053	cytochrome-c oxida
39	85	5.2	227	2 T11250	cytochrome-c oxida
40	84.5	5.2	752	2 E72616	hypothetical prote
41	84	5.2	227	2 I61843	cytochrome-c oxida
42	84	5.2	227	2 T11860	cytochrome-c oxida
43	84	5.2	227	2 T11366	cytochrome-c oxida
44	84	5.2	227	2 T11431	cytochrome-c oxida
45	84	5.2	1482	2 S13495	pregnancy zone pro

## ALIGNMENTS

RESULT 1  
A47003  
cytokine receptor family class II protein CRF2-4 precursor - human  
C:Species: Homo sapiens (man)  
C:Date: 09-Sep-1994 #sequence\_revision 09-Sep-1994 #text\_change 01-Dec-2000  
C:Accession: A47003; G01418  
R:Luftfalia, G.; Gardner, K.; Uze, G.  
Genomics 16, 366-373, 1993  
A:Title: A new member of the cytokine receptor gene family maps on chromosome 21 at 1  
A:Reference number: A47003; M01D:93300510  
A:Accession: A47003  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-325 <LUT>  
A:Cross-references: GB:117227; NID:9393378; PIDN:CAA78933.1; PID:9393379  
R:Luftfalia, G.  
submitted to the EMBL Data Library, April 1994  
A:Reference number: G06935  
A:Accession: G01418  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-123, 'D', 125-268, 'VGRME' <LU2>  
A:Cross-references: EMBL:U08988; NID:9571295; PID:9571296  
C:Genetics:  
A:Gene: GDB:CRF4; CRF2-4  
A:Cross-references: GDB:138168; OMIM:123889  
A:Map position: 21q; 21q22.1-21q22.2  
A:Introns: 17/1; 58/2; 111/1; 166/3; 216/1  
C:Keywords: transmembrane protein

Query Match 11.7% Score 191; DB 2; Length 325;  
Best Local Similarity 26.6%; Pred. No. 1.3e-09;  
Matches 77; Conservative 47; Mismatches 117; Indels 48; Gaps 16;

QY	12	WTSIFMFVFAIICLLDEVAIIIPAPONLSVLSFNKHLIM-SPIVAPGEFYVSVEY 70
DB	3	W-SLGSW---LGGCLVSAAGWVPPEPNRMSVNFENIIQWSPAPAKG-----NLTF 52
QY	71	QGESESYTHSIWIPSSMCSLTEGPCDVTDDITATVPYNRVNRTAGSOTSAA-SILKH 129
DB	53	TAQYLSLR-----IFQDKAMTITLTCDFS-SLSKYGDIHVRNREFADEHSDWNIIFC 106
QY	130	PFNRNSTILTRPGMEIKKXGFHLVIELEDGPOE-----FLVAYWYRE 173
DB	107	PV--DQITLIPGQVQVLEADSL--HMRFLAPKLENEGETMTMKNVYSMTYVQYW--K 160
QY	174	PGAEHHVKNVRSGGIPVHLETPGPAAYCYAQTFFVAIGYSAFSQTECYE-VQGEAIP 232
DB	161	NGTDEKFOITPOYDFEV-LRNLEPMTTYCYQVGRFLPDRNKAQMSSEPVCEQTHDETVP 219
QY	233	---LVALLFAFVGFMLIVVPLF--VWKGRLLQYSCPPVVLPTLTK 276



Interferon receptor-class II cytokine receptor - mouse

C:Species: Mus musculus (house mouse)

C:Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 11-May-2000

C:Accession: J06311

R:Gibbs, V.C.; Pennica, D.

Gene 186, 97-101, 1997

A:Title: cRF2-4: Isolation of cDNA clones encoding the human and mouse proteins.

A:Reference number: J06311; MUID:9719375

A:Accession: J06311

A:Status: Preliminary

A:Molecule type: mRNA

A:Residues: 1-349 <GTR>

A:Cross-references: GB:U53696

Query Match 10.8%; Score 175.5; DB 2; Length 349;

Best Local Similarity 23.7%; Pred. No. 3.5e-08;

Matches 68; Conservative 47; Mismatches 119; Indels 53; Gaps 13;

23 LIPC-----LTDEVAIIIPAPONTLSVLTNNKRLHLMSPVIAPEGTVYVSEYQGEY 74

1 MAPCVAGMLGFLVLPALGMIPPEKVRNMSVFNKIIQMEVPAPFKMLTFQAQE-SY 59

75 ESLTSHWITSSWCSLTGEGPCDVTDDITATVPYNLRVRLTGSQTSAM-SILKHPNR 133

60 RS-FQDH-----CKRTASTQCDPS-HLSKGYDTVRVRAELADEHSEWVNTFCPV-- 108

134 NSTILTRPGMEIKKXGPHLVIELEDLGPQFE-----FLVAVKXRGPGAE 177

109 EDTIIGPEMQLAESL--ELRPSAPQIENEPETWLNKIDSMAYVQVW--KNGTN 164

178 EHVKNVRSGGIPVHLEMEPGAAYCVKAKQTFKAIQXYSAFSQTCEVEVOGE----- 229

165 EKFOVVSYPDSV-LRNLEPWTTCIQOQGFLLDQNRGENSEPICEKRGNDITPSWIV 223

230 AIPVLALFAVFGMLLVVPLFPYKMGRLLOYSQCPVVLPTLTK 276

224 AIIILVSVLVVFLFLGCFV--LMLIYKTKRKHFRSGTSLPQHILK 267

RESULT 5

Interferon alpha receptor type 1 precursor - bovine

C:Species: Bos primigenius taurus (cattle)

C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 05-Nov-1999

C:Accession: S27387; S33770

R:Monchel-Vielh, E.; Lutfalla, G.; Mogensen, K.E.; Uze, G.

FEBS Lett. 313, 255-259, 1992

A:Title: Specific antiviral activities of the human alpha interferons are determined at

Accession: S27387; MUID:93076908

A:Status: preliminary; nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-560 <MOD>

A:Cross-references: EMBL:X68443; NID:9431; PIDN:CNA48484.1; PID:9432

A:Experimental source: MDBK cells

Biochim. Biophys. Acta 1173, 314-319, 1993

A:Title: Cloning and characterization of a bovine alpha interferon receptor.

A:Reference number: S33770; MUID:93305725

A:Accession: S33770

A:Molecule type: mRNA

A:Residues: 1-421, 'V', 423-560 <LIM>

A:Cross-references: EMBL:L06320; NID:9163187; PIDN:AAA02571.1; PID:9163188

A:Experimental source: Lung

C:Keywords: antiviral; cytokine receptor; transmembrane protein

F:1-24/Domain: signal sequence #status predicted <SIG>

F:25-560/Product: Interferon alpha receptor type 1 #status predicted <MAT>

Query Match 10.1%; Score 164.5; DB 2; Length 560;

Best Local Similarity 21.9%; Pred. No. 6.1e-07;

21 YALIPCLLTDEVAIIIPAPONTLSVLTNNKRLHLMSPVIAPEGTVYVSEYQGEYESTLYT- 79

215 YSPVHCICKITVENLEPPENIEVSQONVYLK-----DYRYANMTPOVOMLHARLK 267

80 ----SHWITSSWCSLTGEGPCDVTDDITATVPYN-----LRVRLTGSQTSAMS-- 125

268 RNPGRNHLV---KWKQI---PDCEWVKTKQCFPQNPQKIGIILRVQASDNDNTSFWSEE 321

126 -----ILKHPRNRNSTILTRPGMEIKKXGPHLVY-----ELEDLGPGREF 165

Matches 70; Conservative 62; Mismatches 136; Indels 51; Gaps 14;

21 YALIPCLLTDEVAIIIPAPONTLSVLTNNKRLHLMSPVIAPEGTVYVSEYQGEYESTLYS 80

215 YSPVHCICKITVENLEPPENIEVSQONVYLK-----DYRYANMTPOVOMLHARLK 267

81 HI-----W-IPSSWCSLTGEGPCDVTDDITATVPYNLRVRLTGSQTSAMSILKHPF 131

268 KIPGNHSDKKWQIIPN--CENVTSTHCVFPPREVSSRGIIYVVRASNGTSEFWSEKEFN 325

132 NRNSTILTRPGM---ELIKKXGPHLVY-----ELEDLGPQ-----FEFLVAVKXRGPGAE 385

326 TEKTTITFPPIVYSKYSTDLSHVSQASESEMSVNOILPLIYETIFMENTSAERK 180

181 KVRSGGIPVHLEMEPGAAYCVKAKQTFVK--AIGXYSAFSQTCEVEVOGE-----GEAIPLV 234

386 LEKRTNIT---FPLKRLIYVCVAKRALIENDRNKSSFSFDYCEKRPNTSKTWIIV 442

235 LALFAVGMILIVVPLFPYKMGRLLOYSQCPVVLPTLTK--ITNSPQR--LISCRR 290

443 GTCALFSIPVYIVVSVFL----RCVKYVFEPPSKPPSSVDEYFSDQPLRNLLSTSEE 498

291 EVDAC-----ATAMSPDE 304

499 QTERCFIENASITTEIE 517

RESULT 6

Interferon alpha/beta receptor precursor - human

C:Species: Homo sapiens (man)

C:Date: 22-Jun-1990 #sequence\_revision 22-Jun-1990 #text\_change 22-Oct-1999

C:Accession: A32694; S17112

R:Uze, G.; Lutfalla, G.; Gresser, I.

Cell 60, 225-234, 1990

A:Title: Genetic transfer of a functional human interferon alpha receptor into mouse

A:Reference number: A32694; MUID:90124632

A:Accession: A32694

A:Molecule type: mRNA

A:Residues: 1-557 <UZE>

A:Cross-references: GB:003171; NID:9184645; PIDN:AAA52730.1; PID:9306914

R:Lutfalla, G.

submitted to the EMBL Data Library, July 1991

A:Description: The structure of the human interferon alpha/beta receptor gene.

A:Reference number: S17112

A:Accession: S17112

A:Molecule type: DNA

A:Residues: 1-16, 'A', 18-329, 'V', 343-557 <LUT>

A:Cross-references: EMBL:X60459; NID:932671

C:Genetics:

A:Gene: GDB:IFNAR1; IFNAR: IFNRC

A:Cross-references: GDB:120078; OMIM:107450

A:Map position: 21q22.1-21q22.1

A:Introns: 26/1; 67/2; 126/1; 177/3; 225/1; 263/2; 342/1; 381/3; 432/1; 480/3

C:Keywords: cytokine receptor; glycoprotein; transmembrane protein

F:1-21/Domain: transmembrane #status predicted <TRM1>

F:437-455/Domain: transmembrane #status predicted <TRM2>

F:50,58,81,88,110,172,254,313,314,376,416,453,507,518,537/Binding site: carbohydrate

Query Match

Best Local Similarity 22.0%; Score 162.5; DB 2; Length 557;

Matches 71; Conservative 54; Mismatches 115; Indels 83; Gaps 17;

21 YALIPCLLTDEVAIIIPAPONTLSVLTNNKRLHLMSPVIAPEGTVYVSEYQGEYESTLYT- 79

215 YSPVHCICKITVENLEPPENIEVSQONVYLK-----DYRYANMTPOVOMLHARLK 267

80 ----SHWITSSWCSLTGEGPCDVTDDITATVPYN-----LRVRLTGSQTSAMS-- 125

268 RNPGRNHLV---KWKQI---PDCEWVKTKQCFPQNPQKIGIILRVQASDNDNTSFWSEE 321

126 -----ILKHPRNRNSTILTRPGMEIKKXGPHLVY-----ELEDLGPGREF 165

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Db      322 IKFDTFQALPVPVFIKRS-----LSDFHIYICAPKSGMTVPVIQDPLTE- 370
OY      166 LVAYWKEPQAEHVKVSGGIPVHLEMEPGAAYCAKAO--TFVYAIQXYSFASOTEC 223
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      371 -IIFEMTNSAERKIIETKT---DVTVPNLKPLVYCVKRAAHIMDEKLNSSVFSDDVC 426
OY      224 VEQO-GEAIPLVIALFVFGFMILVVPVLFVWKMGRLLQYSCPPVVLPTLTKTNS-- 280
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      427 EKTKPGMTSKRWL---IVGICIALFALPFIYIAKVELR--CINVEFFP-SLKPSISID 479
OY      281 -----PQR--LISCREEDVAC 295
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      480 EYSEOPLNLLSTSEQIEKC 502

```

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RESULT 7
A:Accession: A49947
Interferon gamma receptor beta subunit - human
N:Alternate names: IFN-gamma R beta chain; IFN-gamma R species-specific cofactor; type 1
C:Species: Mus musculus (house mouse)
C:Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
C:Accession: A49947
R:Hemmi, S.; Bohni, R.; Stark, G.; Di Marco, F.; Aguet, M.
Cell 76, 803-810, 1994
A:Title: A novel member of the interferon receptor family complements functionality of
A:Reference number: A49947; MUID:94170381
A:Accession: A49947
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-332 <HEM>
A:Cross-references: GB:S69336; NID:9545841; PIDN:AA30165.1; PID:9545842
A:Experimental source: early B-cell line Y16
A:Note: sequence extracted from NCBI backbone (NCBIN:145654, NCBI:145656)
C:Keywords: cytokine receptor

```

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Query Match      9.6%; Score 157; DB 2; Length 332;
Best local Similarity 27.0%; Pred. No. 1.5e-06;
Matches 72; Conservative 34; Mismatches 101; Indels 60; Gaps 17;

OY      17 MFFPVALIPCLL-----TDEVALIPAPQNLVSLTMKHLMLMSPIAIGETVY 66
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      6 LW-----LPCLLGLGGAASSPSFSQLAAPLNPRLHLNDEQILTWEP--SPSSNDPR 58
OY      67 SVEQGEYESLYTSHWIPSSWCSLTGEPED-DVTD--DITA-----TVPYN--LRV 113
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      59 PYYQVQVYS-----FIDGSMHLLP-PNCTDITETKCDLTGGRLKLFPHPTVFLRV 110
OY      114 RATLGQTSAMSLIKHPNRSITLTPR--GMEIXKXGFHLVLEL--DL--GPOEFL 166
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      111 RAKRGNLTSMKWGLE-PFOHYENTVGPBKNIISTVPGKSLVHIFSPDFVGHGATFQYL 169
OY      167 VAYWKEPQAEHVKVSGGIPVHLEMEPGAAYCAKAOV---KAIGXYSANSQT 221
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      170 VHWKEKETQEOVEGPFKSNIV--LGNLKPVRVYCLQTEADILKNNKIRPHGLLSNV 227
OY      222 EGYEVOGEA-----PPLVLAFAV 241
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      228 SCHETTANASARLAQVILLIPGIFALL 254

```

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RESULT 8
I56215
Interleukin-10 receptor - human
C:Species: Homo sapiens (man)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 28-Jul-2000
C:Accession: I56215
R:Lin, Y.; Wei, S.H.; Ho, A.S.; de Waal Malefyt, R.; Moore, K.W.
J. Immunol. 152, 1821-1829, 1994
A:Title: Expression cloning and characterization of a human IL-10 receptor.
A:Reference number: I56215; MUID:94165477
A:Accession: I56215

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A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-578 <RES>
A:Cross-references: EMBL:U00672; NID:9482802; PIDN:AA17896.1; PID:9482803
C:Genetics:
A:Gene: GDB:IL10R; HIL-10R
A:Cross-references: GDB:330958; OMIM:146933
A:Map position: 11q23.3-11q23.3
C:Superfamily: interleukin-10 receptor IL10R
C:Keywords: cytokine receptor

```

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Query Match      8.4%; Score 136; DB 2; Length 578;
Best local Similarity 23.8%; Pred. No. 0.00023;
Matches 70; Conservative 47; Mismatches 109; Indels 68; Gaps 14;

OY      23 LIPCLLTDEVAL-----LPAPQNLVSLTMKHLMLMSPIAIGETVY 69
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      1 MLPCLVLLAALLSLRLGSDAHGTLPSPSVWFEAEFFHILHMTPIPNQSESTCYEVA 60
OY      70 YQGEYESLYTSHWIPSSWCSLTGEPED-VYDDITATVPYMLRVATLGQTSAMSLIK 128
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      61 L-----LRYGIESNMSISNCSQTLSDYDLATVLDLYHSNGYRAARAVDGRSHSNWTYVN 115
OY      129 HPNRSNITLT--RPGMEIXKXGFHL-VIEL-----EDLGPQF-EFLVAYWXR 172
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      116 TRFSVDEVTLTGVSYNLTEHN-GFIIIGKIQLPKPAKAPANDYESIFSHFREYETAI-RK 173
OY      173 EPG-----AEHVWVNRSGGIPVHLEMEPGAAYCAKAOVTKAIGXYSANSQTEC 223
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      174 VPGNFTFTHKKVKNHFNLSLTSGEV-----GEFCVQVQPSVASSNSKGMKSKEBC 223
OY      224 VEV--QGAIPLVIALFAFV---GFMLLVVVPVLFVWKMGRLLQYSCPPVVL 271
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      224 ISLFRQYFTVTVVILFFAFVLLSGALAVCLALQLYVRRKKL-----PSVLL 271

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RESULT 9
KFRB3
Tissue factor precursor - rabbit
N:Alternate names: coagulation factor III
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jul-2000
C:Accession: J00441; S23681
R:Andrews, B.S.; Rehentulla, A.; Fowler, B.J.; Edgington, T.S.; Mackman, N.
Gene 98, 265-269, 1991
A:Title: Conservation of tissue factor primary sequence among three mammalian species
A:Reference number: J00441; MUID:91200676
A:Accession: J00441
A:Molecule type: mRNA
A:Residues: 1-292 <AND>
A:Cross-references: GB:M55390; NID:9165696; PIDN:AA63469.1; PID:9165697
A:Experimental source: brain
R:Pavashe, A.; Ezekowitz, M.; Lin, T.C.; Horton, R.; Bach, R.; Konigsberg, W.
Thromb. Haemost. 66, 315-320, 1991
A:Title: Molecular cloning, characterization and expression of cDNA for rabbit brain
A:Reference number: S23681; MUID:92081032
A:Accession: S23681
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 33-292 <PAM>
A:Cross-references: EMBL:X53521; NID:91495; PIDN:CAA37597.1; PID:93980170
C:Comment: Tissue factor is an integral membrane glycoprotein that serves as a recept
C:Superfamily: Expression of tissue factor can be induced in a variety of tissues by cert
C:Keywords: blood coagulation; glycoprotein; lipoprotein; thiolester bond; transmembr
F:1-32/Domain: signal sequence #status predicted <SIG>
F:33-292/Product: tissue factor #status predicted <KMT>
F:33-249/Domain: extracellular #status predicted <EXT>
F:250-271/Domain: transmembrane #status predicted <TM>
F:272-292/Domain: intracellular #status predicted <INT>
F:41,114,154,167,182/Binding site: carboxydrate (Asn) (covalent) #status predicted
F:79-87,216-239/Disulfide bonds: #status predicted

```





N:Alternate names: coagulation factor III  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 22-Jun-1999  
C:Accession: JQ1319  
R:Itakayenoki, Y.; Muta, T.; Miyata, T.; Iwanaga, S.  
Biochem. Biophys. Res. Commun. 181, 1145-1150, 1991  
A:Title: cDNA and amino acid sequences of bovine tissue factor.  
A:Reference number: JQ1319; MUID:92109720  
A:Accession: JQ1319  
A:Molecule type: mRNA  
A:Residues: 1-292 <FAK>  
A:Cross-references: GB:S74147; MID:g241438; PIDN:AAB20755.1; PID:g241439  
A:Experimental source: adrenal gland  
A:Note: part of this sequence, including the amino end of the mature protein, was confirmed  
C:Comment: Tissue factor is an integral membrane glycoprotein that serves as a receptor  
C:Comment: Expression of tissue factor can be induced in a variety of tissues by certain  
C:Superfamily: tissue factor  
K:Keywords: blood coagulation; glycoprotein; lipoprotein; thiolester bond; transmembrane  
F:1-35/Domain: signal sequence; #status predicted <SIG>  
F:36-292/Product: tissue factor; #status experimental <AMT>  
F:36-248/Domain: extracellular; #status predicted <EXT>  
F:249-271/Domain: transmembrane; #status predicted <TM>  
F:272-292/Domain: intracellular; #status predicted <INT>  
F:143,153,181/Binding site: carboxylate (Asn) (covalent) #status predicted  
F:181-89,215-238/Disulfide bonds: #status predicted  
F:118,124/Binding site: carboxylate (Thr) (covalent) #status predicted  
F:274/Binding site: palmitate (Cys) (covalent) #status experimental

Query Match	7.0%	Score 114.5	DB 1	Length 292
Best Local Similarity	19.8%	Pred. No. 0.009		
Matches	49	Conservative	39	Mismatches 103
				Indels 57
				Gaps 9

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Oy 40 NLSVYSTWKKHLHMSPIYALGETFYVYSEVOGESESLYTSHI-----NTPSSWCSLTE 93
      | : | | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 43 NITKSTFEKILHEP-----KINHYTYQISPRGLNM--KKKCYTT 85
      | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Oy 94 GPECDVDDITATVPYNLNVRAPLGSOTSAMSLIKHPNPN-----STLIRPGME-T 145
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 86 NTECVTEDEIKVKNARETLAVLSYPADTSSSTQEPFPFNSEPTPLYETMIGPTIOSE 145
      | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Oy 146 KXKGPHVLELED-----LGPQFEFLVYMWKPEPAEYHKNVBSGGI 188
      | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 146 EOVGTKKLVYODARTLVANSASLISLDEYFGKULNTLYIWKASSTGKKKATNTNNG-- 203
      | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Oy 189 PVHLEHTEPGCAVCVKAQTFV--KAIGXYSASFQSECEVVOGEAIPVLALFAFVGMLI 246
      | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 204 --FLIDVDKGENYCPHYQAVILSRVNOKSPESPIKCTSHK--VLTSELEFLIGVML 258
      | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

      247 LVVVPFLV 254
      | : | | | | |
Db 259 VIIIFIV 266
      | : | | | | |

```

RESULT 15  
A32385  
erythropoietin receptor precursor, membrane-bound form - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 28-Sep-1990 #sequence\_revision 05-Apr-1995 #text\_change 22-Jun-1999  
C:Accession: A41686; A32385; S13249  
R:Hino, M.; Tojo, A.; Misawa, Y.; Morii, H.; Takaku, F.; Shibuya, M.  
Mol. Cell. Biol. 11, 5527-5533, 1991  
A:Title: Unregulated expression of the erythropoietin receptor gene caused by insertion  
A:Reference number: A41686; MUID:92017832  
A:Accession: A41686  
A:Molecule type: mRNA  
A:Residues: 1-507 <HIN>  
A:Cross-references: GB:S59388; MID:9237036; PIDN:AA80029.1; PID:9237037  
A:Experimental source: murine erythroleukemia (MEL) cell line F5-5  
R:D'Andrea, A.D.; Lodish, H.F.; Wong, G.G.  
Cell 57, 277-285, 1989  
A:Title: Expression cloning of the murine erythropoietin receptor.  
A:Reference number: A32385; MUID:89195238

A:Accession: A32385  
A:Molecule type: mRNA  
A:Residues: 1-507 <DNA>  
A:Cross-references: GB:004843; NID:g193090; PIDN:AAA37571.1; PID:g309219  
A:Experimental source: murine erythroleukemia (MEL) cells, subclone 745  
R:Kuramochi, S.; Ikawa, Y.; Todokoro, K.  
J. Mol. Biol. 216, 567-575, 1990  
A:Title: Characterization of murine erythropoietin receptor genes.  
A:Reference number: S13249; MUID:91080149  
A:Accession: S13249  
A:Molecule type: DNA; mRNA  
A:Residues: 1-507 <KUR>  
A:Cross-references: EMBL:X53081; NID:g50861; PIDN:CMA37248.1; PID:g50862  
A:Experimental source: murine erythroleukemia K-1 cells  
C:Genetics:  
A:Introns: 39/1; 83/2; 142/1; 194/3; 246/1; 275/2; 304/3  
C:Superfamily: erythropoietin receptor; cytokine receptor homology  
C:Keywords: alternative splicing; cytokine receptor; glycoprotein; transmembrane prot  
F:1-74/Domain: signal sequence #status predicted <SIG>  
F:25-507/Product: erythropoietin receptor #status predicted <MAT>  
F:25-249/Domain: extracellular #status predicted <EXT>  
F:52-238/Domain: cytokine receptor homology <CRS>  
F:250-271/Domain: transmembrane #status predicted <TM>  
F:272-507/Domain: intracellular #status predicted <INT>  
F:52-62, 90-106/Disulfide bonds: #status predicted  
F:75/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match	7.0%;	Score 114;	DB 1;	Length 507;
Best Local Similarity	23.2%;	Pred. No. 0.019;		
Matches	73;	Conservative	39;	Mismatches 98;
			Indels	104;
			Gaps	18;

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0Y 26 CLLDEVAAILDAP-----OULSVLSTNMKIL-MSPVILAPGETV 65
Db 16 CLLAGANMAPSPBLDPDKFESKALLASKSEELCFTQRIEDLVCFWEAASGMDFN 75
0Y 66 YSVYOGESLYSHIMTBSMCSTLEGE-----CDV-TDITATVPYLRYRAT 116
Db 76 YSFYTOLEGEERKS-----CSLQAPTVRGSVRFWCSLPTADISSVPLEIQYTEA 126
0Y 117 LGS-----OTSAMSLIKHPFNBNSTLTLPNGMEIKXGPHULEDEDLPQPEFLVAY 169
Db 127 SGSPRYHRIIHINEVILLDAP-----AGILARRAE-----GSHVLR----- 164
0Y 170 WAREPGA--EHHVAV-----RSGGIPHLEMTMEPGAACYKAQ-----TF-VKA- 211
Db 165 WLPPGAPMTTHIERYDVASGNRAGCQ--RVEYLE-GRTCEVLSNLRGSTRYFAVRAR 222
0Y 212 -----IGXYSAFQOTCEYEQGSAIFLVLALFAFVGFMLILVWVPLFWKMG-----RL 260
Db 223 MAEPFSGFWMSAWSEPAISLTLASDLDELITL-----SLIVLISILLVTLALLSHRT 276
0Y 261 LQYSCCPVWVLPDR 274
Db 277 LQOKIMPEISPEIS 290

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Search completed: October 12, 2001, 16:10:38  
Job time: 115 sec





GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 12, 2001, 16:08:23 ; Search time 12.3 Seconds

(without alignments)  
520.618 Million cell updates/sec

Title: US-09-265-540E-2

Perfect score: 1627

Sequence: 1 MDTFVLEIWTSLFMWF.....VDACAVMSPEELLRAWIS 311

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 197339 seqs, 20590346 residues 197339

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

Issued\_Patents\_AA.\*  
1: /cgn2\_6/ptodata/2/1aa/5A.COMB.pep.\*  
2: /cgn2\_6/ptodata/2/1aa/5B.COMB.pep.\*  
3: /cgn2\_6/ptodata/2/1aa/6A.COMB.pep.\*  
4: /cgn2\_6/ptodata/2/1aa/6B.COMB.pep.\*  
5: /cgn2\_6/ptodata/2/1aa/PCTUS.COMB.pep.\*  
6: /cgn2\_6/ptodata/2/1aa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	191	11.7	325	2	US-08-683-743-4
2	176.5	10.8	337	5	PCT-US94-14277-8
3	162.5	10.0	537	1	US-08-328-256-10
4	162.5	10.0	557	1	US-08-471-454-2
5	162.5	10.0	557	2	US-08-466-974-2
6	162.5	10.0	557	2	US-08-471-453-2
7	162.5	10.0	557	2	US-08-307-588-4
8	157	9.6	332	5	PCT-US94-14277-2
9	146	9.0	223	5	PCT-US94-14277-6
10	138	8.5	553	2	US-08-943-087-14
11	138	8.5	553	2	US-08-943-087-16
12	138	8.5	553	2	US-08-943-087-18
13	138	8.5	553	2	US-08-943-087-20
14	138	8.5	553	2	US-08-943-087-22
15	138	8.5	553	2	US-08-943-087-24
16	138	8.5	553	2	US-08-943-087-26
17	138	8.5	553	2	US-08-943-087-28
18	138	8.5	553	2	US-08-943-087-30
19	138	8.5	553	2	US-08-943-087-32
20	138	8.5	553	2	US-08-943-087-34
21	138	8.5	553	2	US-08-943-087-36
22	138	8.5	553	2	US-08-943-087-38
23	138	8.5	553	2	US-08-943-087-40
24	138	8.5	553	2	US-08-943-087-42
25	138	8.5	553	2	US-08-943-087-44
26	138	8.5	553	2	US-08-943-087-46
27	138	8.5	553	2	US-08-943-087-48

28	138	8.5	553	2	US-08-943-087-48	Sequence 48, Appl
29	137.5	8.5	221	2	US-08-943-087-54	Sequence 54, Appl
30	137.5	8.5	434	1	US-08-328-256-11	Sequence 11, Appl
31	136.5	8.4	436	2	US-08-307-588-5	Sequence 2, Appl
32	136	8.4	578	1	US-08-424-788-5	Sequence 5, Appl
33	136	8.4	578	1	US-08-110-683-2	Sequence 2, Appl
34	136	8.4	578	2	US-08-683-743-2	Sequence 2, Appl
35	136	8.4	578	2	US-08-477-166-2	Sequence 2, Appl
36	136	8.4	578	2	US-08-472-097-2	Sequence 2, Appl
37	136	8.4	578	5	PCT-US93-11638-2	Sequence 2, Appl
38	135.5	8.3	221	2	US-08-943-087-52	Sequence 52, Appl
39	135.5	8.3	221	2	US-08-943-087-58	Sequence 58, Appl
40	134.5	8.3	221	2	US-08-943-087-56	Sequence 56, Appl
41	133.5	8.2	221	2	US-08-943-087-50	Sequence 50, Appl
42	131.5	8.1	221	2	US-08-943-087-60	Sequence 60, Appl
43	131	8.1	200	5	PCT-US94-14277-4	Sequence 4, Appl
44	128.5	7.9	557	1	US-08-424-788-6	Sequence 6, Appl
45	126.5	7.8	408	2	US-08-683-007A-2	Sequence 2, Appl

## ALIGNMENTS

```

RESULT 1
US-08-683-743-4
; Sequence 4, Application US/08683743
; Patent No. 5843697
;
GENERAL INFORMATION:
; APPLICANT: Pestka, Sidney
; APPLICANT: Kotenko, Sergei
; TITLE OF INVENTION: CYTOKINE RECEPTOR SIGNAL TRANSDUCTION
; TITLE OF INVENTION: CHAIN
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSER: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; STREET: Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
;
COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
;
CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/683,743
; FILING DATE: 17-JUL-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 601-1-050
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ. ID NO. 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 325 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; FRAGMENT TYPE:
;
US-08-683-743-4

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Query Match 11.7%; Score 191; DB 2; Length 325;  
Best Local Similarity 26.6%; Pred. No. 1.4e-12;  
Matches 77; Conservative 47; Mismatches 117; Indels 48; Gaps 16;

QY 12 WTSLEWMEFALIPCLITDEVALIPAPONLSVLTNNKHLMM--SPVIAPEGFTYYSVEY 70  
 Db 3 W-SLGSV-----LGGCLLSALGAVPPENMNSVNFKNILQWESPAPAKG-----NLTJE 52  
 QY 71 QGESESYTSHIWIPISSWCSLTEGPECDDVTDDITATVPYNLRVATGSGQTSAM--SLIKH 129  
 Db 53 TAQYLSTR-----IFQKCAHTITTECDFS--SLKSGDHTLRVAFRADEHSDMWNITFC 106  
 QY 130 PFNRNSTILTRPGMEIKXGFFHLYIELEDLGPOFE-----FLVAYWAKRE 173  
 Db 107 PV--DDITIPPGMQVEVLADSL--HMRFLAPKLENEYETMTMKNYNSMTYNYQW--K 160  
 QY 174 PGAEHYKAVRSGGIPVHLEMTMPEGAICYKAQTFVKAIGYSAFSQTEVE--VQGEAIP 232  
 Db 161 NGTDEKFOIRPOYDFEV--LRLNEPMTTYCYQVRGFLPDRNKGAGSESPVCEQTHDETVP 219  
 QY 233 ---LVIALPFAVFGFMLLVVPLF--VWKMGRLLOYSCCPVYV--PDITLK 276  
 220 SMWAVATLMASV--FMVCLALLGCFSLIMCVYKTKTVAFSPRNSLPOHLK 267

RESULT 2  
 PCT-US94-14277-8  
 ; Sequence 8, Application PC/TUS9414277  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Aguet, Michel  
 ; APPLICANT: Bohni, Ruth  
 ; APPLICANT: Hemmi, Silvio  
 ; TITLE OF INVENTION: Receptor Subunit Polypeptides  
 ; NUMBER OF SEQUENCES: 8  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Genentech, Inc.  
 ; STREET: 460 Point San Bruno Blvd  
 ; CITY: South San Francisco  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 94060  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: patin (Genentech)  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: PCT/US94/14277  
 ; FILING DATE: 07-DEC-1994  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/164596  
 ; FILING DATE: 09-DEC-1993  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Love, Richard B.  
 ; REGISTRATION NUMBER: 34,659  
 ; REFERENCE/DOCKET NUMBER: 866PCT  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 415/225-5530  
 ; TELEFAX: 415/952-9881  
 ; TELEX: 910/371-7168  
 ; INFORMATION FOR SEQ ID NO: 8:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 337 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; PCT-US94-14277-8

Query Match 10.8%; Score 176.5; DB 5; Length 337;  
 Best Local Similarity 25.8%; Pred. No. 5.5e-11;  
 Matches 74; Conservative 43; Mismatches 123; Indels 47; Gaps 14;  
 QY 11 WTSLEWMEFALIPCLITDEVALIPAPONLSVLTNNKHLMMSPVIAPEGFT--VYYSV 68  
 Db 6 LMSLLILGFAFAAAAPPPQLSOLPAPQHPKIRLYNAEOVLSWEPVALSNSTRFVYQV 65

QY 69 EYQGESESYTSHIWIPISSWCSLTEGPECDDVTDDITATVP-----YNLRVATIGS 119  
 Db 66 QEKYDSKWFETADISIGVNCITATATEC-----DETAASPSAGFPMDFNVTLRRLAEIGA 121  
 QY 120 QTSAMSLI---KHPNRNSTILTRPGMETKXGFFHLYI-----ELEDLGPOFE--FLVAY 169  
 Db 122 LHSAAVTMPWFQH--YRNVTVGPPENIEVTPEGSLITREFSSPFDIADTSTAFPCYVHY 179  
 QY 170 WAREPAAEHK--MYRSGGIPVHLEMTMPEGAICYKAQ-----TFVKAIGYSAFSQT 221  
 Db 180 W--EKGGIOQVKGPRNSI--SLDNKPSRYCCIQVQAQOLMKNNSNIFRVGHLNIS-- 233  
 QY 222 ECVEVQGA--IPVIALPFAVFGFMLLVVPP---LFWKMGRLLOY 263  
 Db 224 -CYDTMADASTELQOVILISVCTFSLLSYLAGACFVLKYGYGLIKY 279

RESULT 3  
 US-08-328-256-10  
 ; Sequence 10, Application US/08328256  
 ; Patent No. 5643749  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Revel, Michel  
 ; APPLICANT: ABRAMOVICH, Carolina  
 ; APPLICANT: RATOVIJSKI, Edward  
 ; TITLE OF INVENTION: SOLUBLE INTERFERON ALPHA-RECEPTOR, ITS  
 ; PREPARATION AND USE  
 ; NUMBER OF SEQUENCES: 12  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: BROWDY AND NEIMARK  
 ; STREET: 419 Seventh Street, N.W., Suite 300  
 ; CITY: Washington  
 ; STATE: D.C.  
 ; COUNTRY: USA  
 ; ZIP: 20004  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patentin Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/328,256  
 ; FILING DATE: 24-OCT-1994  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: IL 107378  
 ; FILING DATE: 24-OCT-1993  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: BROWDY, Roger L.  
 ; REGISTRATION NUMBER: REVEL-13  
 ; REFERENCE/DOCKET NUMBER: 25,618  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 202-628-5197  
 ; TELEFAX: 202-737-3528  
 ; TELEX: 248633  
 ; INFORMATION FOR SEQ ID NO: 10:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 557 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-08-328-256-10

Query Match 10.0%; Score 162.5; DB 1; Length 557;  
 Best Local Similarity 22.0%; Pred. No. 3.7e-09;  
 Matches 71; Conservative 54; Mismatches 115; Indels 83; Gaps 17;  
 QY 21 VALIPCLITDEVALIPAPONLSVLTNNKHLMMSPVIAPEGFTVYYSVEYQGESESYLT- 79  
 Db 215 YSPVHCIRKTYVENLPPPENIEVSQNONYVLKM-----DYTYANMTFQVQMLHAFIAK 267  
 QY 80 ---SHIWIPISSWCSLTEGPECDDVTDDITATVPYN-----LVRVATIGSGTSAMS-- 125

Db 268 RNPGRNHLT---KWKQI---PDCENVKTKQCVFPQVNFQKGIYLLRVQASDGNNTSFWSEE 321  
QY 126 -----ILKHPNRNSTILTRPGMEIKXGPHLYT-----ELEDLGPOFEF 165  
Db 322 IKFPEIQAFLPFPVENIRS-----LSDSFHYIIGAPKQSGNTPVIQDYPLIYE- 370  
QY 166 LVAYWAKREPGEAEHVAVKVRSGGIPVHLETPMEPGAAYCVKAO--TFVKAIGXSAFSQTEC 223  
Db 371 -IIFWENTSNAERKIEKKT---DVTVPNLKPLTVYCVKARAHMTDEKLNKSSVFSDAVC 426  
QY 224 VEOV-GEAIPLYLALFAPVGMILLVVPFLVWKMGRLLQYSCCPVVVLPDTLKTINS-- 280  
Db 427 EKTKEPNTSKIML---IVGICIALFALPFIYIAKVFLL--CINVYFFP-SLKPSSSID 479  
QY 281 -----PQK--LISCREEVDAC 295  
Db 480 EYFSEQPLKNLLSTSEQIEKC 502

## RESULT 4

US-08-471-454-2  
Sequence 2, Application US/08471454

Patent No. 5731169  
GENERAL INFORMATION:  
APPLICANT: MOGENSEN, Knud E.  
APPLICANT: UZE, Gilles  
APPLICANT: LUTFALLA, Georges  
APPLICANT: GRESSER, Ion  
TITLE OF INVENTION: CDNA FRAGMENT CODING FOR THE GENE FOR  
TITLE OF INVENTION: THE ALPHA INTERFERON RECEPTOR AND PROCESS FOR THE  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NIXON & VANDERHAYE P.C.  
STREET: 1100 NORTH GLEBE ROAD  
CITY: ARLINGTON  
STATE: VIRGINIA  
COUNTRY: U.S.A.  
ZIP: 22201-4714  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/471.454  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/900,642  
FILING DATE: 15-JUN-1992  
APPLICATION NUMBER: FR 89/13770  
ATTORNEY/AGENT INFORMATION:  
NAME: BYRNE, THOMAS E.  
REGISTRATION NUMBER: 32,205  
REFERENCE/DOCKET NUMBER: 960-7  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 816-4000  
TELEFAX: (703) 816-4100  
TELEX: 200797 NIXN UR  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 557 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-471-454-2

Query Match 10.0%; Score 162.5; DB 1; Length 557;

Best Local Similarity 22.0%; Pred. No. 3.7e-09;  
Matches 71; Conservative 54; Mismatches 115; Indels 83; Gaps 17;

QY 21 VALIPCLLDEVAAILAPQNLSTVSTNMKLLMMSPIVIAAGEFVYYSVEYQGEYESLYT- 79  
Db 215 YSPVHCIKTTEVELELPPEIEIYSQNONVYLMK-----DITYANMTQVOMLHAFK 267  
QY 80 ----SHIWISSWCSLTGEPCCDVTDDITATVYN-----LVRPATIGSOTSAMS- 125  
Db 268 RNPGRNHLT---KWKQI---PDCENVKTKQCVFPQVNFQKGIYLLRVQASDGNNTSFWSEE 321  
QY 126 -----ILKHPNRNSTILTRPGMEIKXGPHLYT-----ELEDLGPOFEF 165  
Db 322 IKFPEIQAFLPFPVENIRS-----LSDSFHYIIGAPKQSGNTPVIQDYPLIYE- 370  
QY 166 LVAYWAKREPGEAEHVAVKVRSGGIPVHLETPMEPGAAYCVKAO--TFVKAIGXSAFSQTEC 223  
Db 371 -IIFWENTSNAERKIEKKT---DVTVPNLKPLTVYCVKARAHMTDEKLNKSSVFSDAVC 426  
QY 224 VEOV-GEAIPLYLALFAPVGMILLVVPFLVWKMGRLLQYSCCPVVVLPDTLKTINS-- 280  
Db 427 EKTKEPNTSKIML---IVGICIALFALPFIYIAKVFLL--CINVYFFP-SLKPSSSID 479  
QY 281 -----PQK--LISCREEVDAC 295  
Db 480 EYFSEQPLKNLLSTSEQIEKC 502

## RESULT 5

US-08-466-974-2  
Sequence 2, Application US/08466974  
Patent No. 5861258

GENERAL INFORMATION:  
APPLICANT: MOGENSEN, Knud E.  
APPLICANT: UZE, Gilles  
APPLICANT: LUTFALLA, Georges  
APPLICANT: GRESSER, Ion  
TITLE OF INVENTION: CDNA FRAGMENT CODING FOR THE GENE FOR  
TITLE OF INVENTION: THE ALPHA INTERFERON RECEPTOR AND PROCESS FOR THE  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NIXON & VANDERHAYE P.C.  
STREET: 1100 NORTH GLEBE ROAD  
CITY: ARLINGTON  
STATE: VIRGINIA  
COUNTRY: U.S.A.  
ZIP: 22201-4714  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/466.974  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/900,642  
FILING DATE: 15-JUN-1992  
APPLICATION NUMBER: FR 89/13770  
ATTORNEY/AGENT INFORMATION:  
NAME: BYRNE, THOMAS E.  
REGISTRATION NUMBER: 32,205  
REFERENCE/DOCKET NUMBER: 960-7  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 816-4000  
TELEFAX: (703) 816-4100  
TELEX: 200797 NIXN UR  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 557 amino acids



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; APPLICATION NUMBER: PCT/EP93/00770
; FILING DATE: 30-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 92400902.0
; FILING DATE: 31-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Saxe, Bernhard D.
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 17283/117/GUPL
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 557 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-307-588-4

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Query Match          10.0% Score 162.5; DB 2; Length 557;
Best Local Similarity 22.0%; Pred. No. 3.7e-09;
Matches 71; Conservative 54; Mismatches 115; Indels 83; Gaps 17;

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QY 21 YALPCLTDEVALPAPONLSVLTNNKHLMSVPVIAPEFTVYSVEYGEYESLYT- 79
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; : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 215 YSPHCITVTENELPPENIEVSQNCNYLKW-----DYTANNMFGQWLHAFLK 267
; : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 80 ----SHWIPSSWCSLTGPECDYTDITATVPVY-----LNRATLSQTSAMS- 125
; : : : : : : : : : : : : : : : : : : : : : : : : : : : :
; : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 268 RNPNNHLY---KMKQI---PCDENKTKQCVFPQNVFQKGIYLLHVOASDGNNTSFWSE 321
; : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 126 -----LTKRPNNSTILRRPGMEIKKGFHLVY-----ELEDLGPOEEF 165
; : : : : : : : : : : : : : : : : : : : : : : : : : : : :
; : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 322 IKPTEIQAFLPPVFNIRS-----LSDSFHITIGAPKOSGNTPVTDYPLITE- 370
; : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 166 LVAYMKEPAAEEHVKMWSGGIPVHLEMPGAAYCVKAQ--TFVKAIGXSAFSQTEC 223
; : : : : : : : : : : : : : : : : : : : : : : : : : : : :
; : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 371 -IITWENTSNAERKIIETK---DYTVNKLPLTYCYKAKRAHTDEKLKSSVSDAVC 426
; : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 224 VEVO-GEAIPVLALFAVGMILVVVPLFVWKGRLQYSCCPVVVLPDLTKITNS-- 280
; : : : : : : : : : : : : : : : : : : : : : : : : : : : :
; : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 427 EKTSPGNTSKIML-----IVGICIALFALPFIYIAKAVFLR--CINYPVEFP-SLKRSSSID 479
; : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 281 -----PQK--LISCRREEVDAC 295
; : : : : : : : : : : : : : : : : : : : : : : : : : : : :
; : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 480 EYFSEQPLKNLLSTSEQIEKC 502

```

```

; RESULT 8
; PCT-US94-14277-2
; Sequence 2, Application PC/TUS9414277
; GENERAL INFORMATION:
; APPLICANT: Aguet, Michel
; APPLICANT: Bohml, Ruth
; APPLICANT: Hemmi, Silvio
; TITLE OF INVENTION: Receptor Subunit Polypeptides
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/14277

```

```

; FILING DATE: 07-DEC-1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/164596
; FILING DATE: 09-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: 866PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/425-5530
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 332 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; PCT-US94-14277-2

```

```

Query Match          9.6% Score 157; DB 5; Length 332;
Best Local Similarity 27.0%; Pred. No. 6.9e-09;
Matches 72; Conservative 34; Mismatches 101; Indels 60; Gaps 17;

```

```

QY 17 MNEFYALIPCLL-----TDEVALIPAPONLSVLTNNKHLMSVPVIAPEFTVY 66
; : : : : : : : : : : : : : : : : : : : : : : : : : : : :
; : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 6 LW-----LPSLLLCGGAASSPDSFSQLAAPLNPRHLHYNDQIILTWEP--SPSSNDPR 58
; : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 67 SVEYGEYESLYTSHWIDSSWCSLTGEPBC-DVTD---DITA-----TVPNY--LRV 113
; : : : : : : : : : : : : : : : : : : : : : : : : : : : :
; : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 59 PVYQYEYS-----FIDGSMHRLLE-PNCTDITEKCDLTGGRLKLPHPFTVELRV 110
; : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 114 RATIGQTSAMSLTKRPFNRNSTIILTRP--GMEIXKXGFHLVLELE---DL--GPOEFL 166
; : : : : : : : : : : : : : : : : : : : : : : : : : : : :
; : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 111 RAKRGMLTSKWGLE--PFGHYENVTVGPKNISVTPGKSLVTHFSPPFVFGATFOYL 169
; : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 167 VAYMKEPAAEEHVK-MVNSGGIPVHLEMPGAAYCVKAQTFV---KAIGXSAFSQTEC 221
; : : : : : : : : : : : : : : : : : : : : : : : : : : : :
; : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 170 VHWKESSEYQOEVEEPFSNSTIV--LGNLKPRRYVICIQTEADILKNNKIRPHGLSNV 227
; : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 222 ECEVOGEA-----IPVLALFAV 241
; : : : : : : : : : : : : : : : : : : : : : : : : : : : :
; : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 228 SCHEFTANASARLQYILPLIGIFALL 254

```

```

; RESULT 9
; PCT-US94-14277-6
; Sequence 6, Application PC/TUS9414277
; GENERAL INFORMATION:
; APPLICANT: Aguet, Michel
; APPLICANT: Bohml, Ruth
; APPLICANT: Hemmi, Silvio
; TITLE OF INVENTION: Receptor Subunit Polypeptides
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/14277
; FILING DATE: 07-DEC-1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/164596

```





APPLICATION NUMBER: US/08/943,087  
FILING DATE:  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/803,305  
FILING DATE: 20-FEB-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Lunn, Paul G  
REGISTRATION NUMBER: 32,743  
REFERENCE/DOCKET NUMBER: 96-24C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-442-6627  
TELEFAX: 206-442-6678  
TELEX:  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 553 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: internal  
US-08-943-087-18

Query Match 8.5%; Score 138; DB 2; Length 553;  
Best Local Similarity 21.3%; Pred. No. 1.7e-06;  
Matches 55; Conservative 43; Mismatches 98; Indels 62; Gaps 11;

QY 24 IPCLLTDEVALIPAPONLSVLTNNKHLMMSPVIA-PGETVYYSVYQGEYESLYTSHI 82  
DB 30 VPCVSGSGLPKRPAITFLSLNNKNTLQMTPEGLQGVKVTYVOY-----FTYQKK 80  
QY 83 WIPSSWCSLTEGPCEDVTDIT-ATVPYNLRVRATLSQTSAM--SILKHPNNR----- 134  
DB 81 WLKSECRNINRYCDLSAETSDYEHQYAKVKAIMGTKSKMAESGRFYPLETQIGPP 140  
QY 135 -----STILTRPGMEIKKGFHLVIELEDLGPQEFVLAV-----WKREPG 175  
DB 141 EVALTDEKSI SVLTAP-EKMRNPEDLPVSMQOISNLTKNVSVLTKSNRTWSQ--C 197  
QY 176 AEHVKNVRSRGIPVHETMEPGAAYCYKQTFVKAIGXYSAFSQTCEVEQGE----- 229  
DB 198 VTNHTLV-----LWLEPNTLYCVHVESFVGPPIRRAPQSEKOCARTLKQSSSEFK 248  
QY 230 -----AIPVLALPAF 240  
DB 249 AKIIFWVLPISITVFLF 266

RESULT 14  
US-08-943-087-20  
Sequence 20, Application US/08943087  
Patent No. 5945511  
GENERAL INFORMATION:  
APPLICANT: Lok, SI  
APPLICANT: Kho, Choon J.  
APPLICANT: Jelmeberg, Anna C.  
APPLICANT: Adams, Robyn L.  
APPLICANT: Whitmore, Theodore E.  
APPLICANT: Fairrah, Theresa M.  
TITLE OF INVENTION: CYTOKINE RECEPTOR  
NUMBER OF SEQUENCES: 60  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Zymogenetics, Inc.  
STREET: 1201 Eastlake Avenue East  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98102  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/943,087  
FILING DATE:  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/803,305  
FILING DATE: 20-FEB-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Lunn, Paul G  
REGISTRATION NUMBER: 32,743  
REFERENCE/DOCKET NUMBER: 96-24C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-442-6627  
TELEFAX: 206-442-6678  
TELEX:  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 553 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: internal  
US-08-943-087-20

Query Match 8.5%; Score 138; DB 2; Length 553;  
Best Local Similarity 21.3%; Pred. No. 1.7e-06;  
Matches 55; Conservative 43; Mismatches 98; Indels 62; Gaps 11;

QY 24 IPCLLTDEVALIPAPONLSVLTNNKHLMMSPVIA-PGETVYYSVYQGEYESLYTSHI 82  
DB 30 VPCVSGSGLPKRPAITFLSLNNKNTLQMTPEGLQGVKVTYVOY-----FTYQKK 80  
QY 83 WIPSSWCSLTEGPCEDVTDIT-ATVPYNLRVRATLSQTSAM--SILKHPNNR----- 134  
DB 81 WLKSECRNINRYCDLSAETSDYEHQYAKVKAIMGTKSKMAESGRFYPLETQIGPP 140  
QY 135 -----STILTRPGMEIKKGFHLVIELEDLGPQEFVLAV-----WKREPG 175  
DB 141 EVALTDEKSI SVLTAP-EKMRNPEDLPVSMQOISNLTKNVSVLTKSNRTWSQ--C 197  
QY 176 AEHVKNVRSRGIPVHETMEPGAAYCYKQTFVKAIGXYSAFSQTCEVEQGE----- 229  
DB 198 VTNHTLV-----LWLEPNTLYCVHVESFVGPPIRRAPQSEKOCARTLKQSSSEFK 248  
QY 230 -----AIPVLALPAF 240  
DB 249 AKIIFWVLPISITVFLF 266

RESULT 15  
US-08-943-087-22  
Sequence 22, Application US/08943087  
Patent No. 5945511  
GENERAL INFORMATION:  
APPLICANT: Lok, SI  
APPLICANT: Kho, Choon J.  
APPLICANT: Jelmeberg, Anna C.  
APPLICANT: Adams, Robyn L.  
APPLICANT: Whitmore, Theodore E.  
APPLICANT: Fairrah, Theresa M.  
TITLE OF INVENTION: CYTOKINE RECEPTOR  
NUMBER OF SEQUENCES: 60  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Zymogenetics, Inc.  
STREET: 1201 Eastlake Avenue East  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98102



COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/943.087  
FILING DATE:  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/803.305  
FILING DATE: 20-FEB-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Lann, Paul G  
REGISTRATION NUMBER: 32,743  
REFERENCE/DOCKET NUMBER: 96-24C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-442-6627  
TELEFAX: 206-442-6678  
TELEX:  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 553 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: internal  
US-08-943-087-22

Query Match 8.5%; Score 138; DB 2; Length 553;  
Best Local Similarity 21.3%; Pred. No. 1.7e-06;  
Matches 55; Conservative 43; Mismatches 98; Indels 62; Gaps 11;

QY 24 IPCLTDEVAIIAPQNLSTNKKHLMSPVIA-PGETVYYSVEYQGEYESLYTSHI 82  
DB 30 VPCVSGG---LPKPANITFLSNMKNVLOWTPPEGLGKVTYTVQY-----FIYQKK 80

QY 83 WIPSSWCSLTGEGEDVDITF-ATVPYNLRVRAITLGSQTSAM--SILKHPFNRN----- 134  
DB 81 WLNKSECRNINFTYCDLSNEDSYEHQYAKYKALMGTKCSKMAESGRFPPELETQIGPP 140

QY 135 -----STLIRPGMEIYKXGFHLYIELEDLGPOFEFLVAY-----WAREPG 175  
DB 141 EVALTDEKSIYVLTAP-EKKRNPEDLPSMQIYSNLKYNVSLNTKSNRTWSQ--C 197

QY 176 AEEHYKAVRSIGIPVHLETMEPGAAYCYKAQTFVKAIGYSAFSQTECEVOGE----- 229  
DB 198 VTNHTLV-----LTWLEPNFLYCVHVESFVGPFRRAQPSKOCARTLKQSSFEK 248

QY 230 -----AIPLVALLFAF 240  
DB 249 AKIIFWVLPISITVLELF 266

Search completed: October 12, 2001, 16:10:15  
Job time: 112 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compen Ltd.

OK protein - protein search, using sw model

Run on: October 12, 2001, 16:06:48 ; Search time 20.8 Seconds  
(without alignments)  
906.445 Million cell updates/sec

Title: US-09-265-540E-2  
Perfect score: 1627  
Sequence: 1 MORTWVLEIWTSLFMWF.....VDACATVMSPEELLRAWIS 311

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues  
Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0  
Maximum DB seq length: 200000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: A.Geneseq\_0601.\*  
2: /SID8/gcgdata/geneseq/geneseq/AA1980.DAT.\*  
3: /SID8/gcgdata/geneseq/geneseq/AA1981.DAT.\*  
4: /SID8/gcgdata/geneseq/geneseq/AA1982.DAT.\*  
5: /SID8/gcgdata/geneseq/geneseq/AA1983.DAT.\*  
6: /SID8/gcgdata/geneseq/geneseq/AA1984.DAT.\*  
7: /SID8/gcgdata/geneseq/geneseq/AA1985.DAT.\*  
8: /SID8/gcgdata/geneseq/geneseq/AA1986.DAT.\*  
9: /SID8/gcgdata/geneseq/geneseq/AA1987.DAT.\*  
10: /SID8/gcgdata/geneseq/geneseq/AA1988.DAT.\*  
11: /SID8/gcgdata/geneseq/geneseq/AA1989.DAT.\*  
12: /SID8/gcgdata/geneseq/geneseq/AA1990.DAT.\*  
13: /SID8/gcgdata/geneseq/geneseq/AA1991.DAT.\*  
14: /SID8/gcgdata/geneseq/geneseq/AA1992.DAT.\*  
15: /SID8/gcgdata/geneseq/geneseq/AA1993.DAT.\*  
16: /SID8/gcgdata/geneseq/geneseq/AA1994.DAT.\*  
17: /SID8/gcgdata/geneseq/geneseq/AA1995.DAT.\*  
18: /SID8/gcgdata/geneseq/geneseq/AA1996.DAT.\*  
19: /SID8/gcgdata/geneseq/geneseq/AA1997.DAT.\*  
20: /SID8/gcgdata/geneseq/geneseq/AA1998.DAT.\*  
21: /SID8/gcgdata/geneseq/geneseq/AA2000.DAT.\*  
22: /SID8/gcgdata/geneseq/geneseq/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1620	99.6	311	20	AAV41736 - <i>act</i>
2	1620	99.6	311	21	AAAB44292 - <i>act</i>
3	1620	99.6	311	21	AAAB34440 - <i>act</i>
4	1620	99.6	311	21	AAAY97046 - <i>act</i>
5	1620	99.6	311	21	AAAY46664 - <i>act</i>
6	1620	99.6	311	21	AAAB66676 - <i>act</i>
7	1620	99.6	311	22	AAAB65199 - <i>act</i>
8	1619	99.5	311	22	AAAY39472 - <i>act</i>
9	1243	76.4	308	21	AAAY97048 - <i>act</i>
10	529	32.5	100	21	AAAG03609 - <i>act</i>
11	191	11.7	325	19	AAW52296 - <i>act</i>

12	191	11.7	325	22	AAAB31214	Amino acid sequenc
13	179.5	11.0	337	16	AAAB71035	Human IFN-gamma ac
14	176.5	10.8	337	13	AAAB75783	IFN-gamma receptor
15	163.5	10.0	557	13	AAAB28496	Sequence of a soul
16	162.5	10.0	557	12	AAAB19558	Human alpha-interf
17	162.5	10.0	557	12	AAAB14488	Complete Interfero
18	162.5	10.0	557	14	AAAB2635	Human Interferon r
19	162.5	10.0	557	16	AAAB21804	Transmembranl int
20	162.5	10.0	557	21	AAAB57094	Human prostate can
21	161.5	9.9	557	16	AAAB75356	Human IFN receptor
22	157	9.6	332	16	AAAB75782	IFN-gamma receptor
23	138	8.5	533	19	AAAB79159	Zeylor7 cytokine r
24	137.5	8.5	434	16	AAAB21805	Spliced-deleted in
25	136.5	8.4	436	12	AAAB14487	Soluble interferon
26	136.5	8.4	436	13	AAAB28495	Sequence of a soul
27	136	8.4	578	15	AAAB57138	Interleukin-10 rec
28	136	8.4	578	19	AAAB1804	Human IL-10 recept
29	133.5	8.2	436	16	AAAB71723	IFN receptor extra
30	132	8.1	263	18	AAAB17725	Human tissue facto
31	129	7.9	263	18	AAAB17742	Human tissue facto
32	129	7.9	263	18	AAAB17743	Human tissue facto
33	128	7.9	263	18	AAAB17723	Human tissue facto
34	128	7.9	263	18	AAAB17724	Human tissue facto
35	126.5	7.8	235	18	AAAB1867	Human tissue facto
36	126.5	7.8	235	19	AAAB48270	Mature human tissu
37	126.5	7.8	408	20	AAAB4315	Trx-rabbit tissue
38	126	7.7	263	18	AAAB17744	Human tissue facto
39	126	7.7	263	18	AAAB17745	Human tissue facto
40	126	7.7	263	18	AAAB17719	Human tissue facto
41	125.5	7.7	295	9	AAAB1503	Human tissue facto
42	125.5	7.7	295	9	AAAB80504	Sequence encoded b
43	125.5	7.7	295	9	AAAB80713	Complete sequence
44	125.5	7.7	295	15	AAAB5178	Pre-hurFh Homo s
45	125.5	7.7	295	18	AAAB31532	Human tissue facto

# ALIGNMENTS

RESULT 1	AAV41736	standard; Protein; 311 AA.
ID	AAV41736	
XX	AAV41736;	
AC	AAV41736;	
XX		
DT	07-DEC-1999	(first entry)
XX		
DE	Human PRO114	protein sequence.
XX		
KW	Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;	
KW	probe; blood coagulation disorder; cancer; cellular adhesion disorder;	
KW	secreted protein; transmembrane protein.	
XX		
OS	Homo sapiens.	
XX		
PN	W09946281-A2.	
XX		
PD	16-SEP-1999.	
XX		
PF	08-MAR-1999;	99WO-US05028.
XX		
PR	10-MAR-1998;	98US-0077450.
PR	11-MAR-1998;	98US-0077632.
PR	11-MAR-1998;	98US-0077641.
PR	11-MAR-1998;	98US-0077649.
PR	12-MAR-1998;	98US-0077791.
PR	13-MAR-1998;	98US-0078004.
PR	17-MAR-1998;	98US-0040220.
PR	20-MAR-1998;	98US-0078886.
PR	20-MAR-1998;	98US-0078910.
PR	20-MAR-1998;	98US-0078936.
PR	20-MAR-1998;	98US-0078939.
PR	25-MAR-1998;	98US-0079294.

PR 26-MAR-1998; 98US-0079656.  
 PR 27-MAR-1998; 98US-0079663.  
 PR 27-MAR-1998; 98US-0079664.  
 PR 27-MAR-1998; 98US-0079689.  
 PR 27-MAR-1998; 98US-0079728.  
 PR 27-MAR-1998; 98US-0079786.  
 PR 30-MAR-1998; 98US-0079920.  
 PR 30-MAR-1998; 98US-0079923.  
 PR 31-MAR-1998; 98US-0080105.  
 PR 31-MAR-1998; 98US-0080107.  
 PR 31-MAR-1998; 98US-0080165.  
 PR 31-MAR-1998; 98US-0080194.  
 PR 01-APR-1998; 98US-0080327.  
 PR 01-APR-1998; 98US-0080328.  
 PR 01-APR-1998; 98US-0080333.  
 PR 01-APR-1998; 98US-0080334.  
 PR 08-APR-1998; 98US-0081049.  
 PR 08-APR-1998; 98US-0081070.  
 PR 08-APR-1998; 98US-0081071.  
 PR 09-APR-1998; 98US-0081195.  
 PR 09-APR-1998; 98US-0081203.  
 PR 09-APR-1998; 98US-0081229.  
 PR 15-APR-1998; 98US-0081817.  
 PR 15-APR-1998; 98US-0081838.  
 PR 15-APR-1998; 98US-0081952.  
 PR 15-APR-1998; 98US-0081955.  
 PR 21-APR-1998; 98US-0082568.  
 PR 21-APR-1998; 98US-0082569.  
 PR 22-APR-1998; 98US-0082700.  
 PR 22-APR-1998; 98US-0082704.  
 PR 22-APR-1998; 98US-0082804.  
 PR 23-APR-1998; 98US-0082767.  
 PR 27-APR-1998; 98US-0082796.  
 PR 28-APR-1998; 98US-0083336.  
 PR 29-APR-1998; 98US-0083392.  
 PR 29-APR-1998; 98US-0083495.  
 PR 29-APR-1998; 98US-0083496.  
 PR 29-APR-1998; 98US-0083499.  
 PR 29-APR-1998; 98US-0083500.  
 PR 29-APR-1998; 98US-0083545.  
 PR 29-APR-1998; 98US-0083554.  
 PR 29-APR-1998; 98US-0083558.  
 PR 30-APR-1998; 98US-0083559.  
 PR 05-MAY-1998; 98US-0083742.  
 PR 06-MAY-1998; 98US-0084414.  
 PR 06-MAY-1998; 98US-0084441.  
 PR 07-MAY-1998; 98US-0084598.  
 PR 07-MAY-1998; 98US-0084600.  
 PR 07-MAY-1998; 98US-0084627.  
 PR 07-MAY-1998; 98US-0084637.  
 PR 07-MAY-1998; 98US-0084639.  
 PR 07-MAY-1998; 98US-0084640.  
 PR 07-MAY-1998; 98US-0084643.  
 PR 13-MAY-1998; 98US-0085323.  
 PR 13-MAY-1998; 98US-0085338.  
 PR 13-MAY-1998; 98US-0085339.  
 PR 15-MAY-1998; 98US-0085573.  
 PR 15-MAY-1998; 98US-0085579.  
 PR 15-MAY-1998; 98US-0085580.  
 PR 15-MAY-1998; 98US-0085582.  
 PR 15-MAY-1998; 98US-0085689.  
 PR 15-MAY-1998; 98US-0085697.  
 PR 15-MAY-1998; 98US-0085700.  
 PR 15-MAY-1998; 98US-0085704.  
 PR 18-MAY-1998; 98US-0086023.  
 PR 22-MAY-1998; 98US-0086392.  
 PR 22-MAY-1998; 98US-0086414.  
 PR 22-MAY-1998; 98US-0086430.  
 PR 22-MAY-1998; 98US-0086486.  
 PR 28-MAY-1998; 98US-0087098.  
 PR 28-MAY-1998; 98US-0087106.

PR 28-MAY-1998; 98US-0087208.  
 PR 30-JUL-1998; 98US-0094651.  
 PR 11-SEP-1998; 98US-0100038.  
 XX  
 PA (GETH ) GENENTECH INC.  
 PI Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;  
 XX  
 DR WPI; 1999-551358/46.  
 DR N-PSDB; AA234190.  
 XX  
 PT New secreted and transmembrane polypeptides, and their polynucleotides,  
 PT useful for treating blood coagulation disorders, cancers and cellular  
 PT adhesion disorders -  
 XX  
 PS Claim 12; Fig 142; 530pp; English.  
 XX  
 CC The present invention describes secreted and transmembrane polypeptides  
 CC and their polynucleotides. The nucleotide sequences are useful as  
 CC sources of probes, primers, for chromosome mapping, and for generation  
 CC of antisense sequences. They can also be used to create transgenic  
 CC animals. The proteins can be used to treat a variety of diseases and  
 CC disorders, depending on their function. Diseases that may be treated  
 CC include blood coagulation disorders, cancers and cellular adhesion  
 CC disorders. They may also be used to raise antibodies. AA23391 to  
 CC AA34338, and AA41685 to AA41774 represent polynucleotide and  
 CC polypeptide sequence given in the exemplification of the present  
 CC invention.  
 XX  
 SQ Sequence 311 AA;

Query Match 99.6%; Score 1620; DB 20; Length 311;  
 Best Local Similarity 98.7%; Pred. No. 6.5e-164;

Matches 307; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 MGTFTMLEEITWLSFMFFYALIPCLLTDEVALIPAPONLSVLTNNKHLMSPTIAP 60  
 DB 1 mgtftmleelwtslfmffyalipclltdevaillpqpnlsvltnmkhlmsptlap 60  
 QY 61 GETVYYSVEYQGEVSLTSHMIRSSMSCLTEGPECDYTDITATVPINLAVRATLSQ 120  
 DB 61 getvyysveyqgeysltshmlrswscsltegspecdytditattvpynlavrattlsq 120  
 QY 121 TSAMGIIKHPFRNSTIITRPCEIXKXGFHVIETEDIGPOFEFLVAVXREPGEAEHY 180  
 DB 121 tsamgiikhpfnrnstiitrpmeltkgfhnvleiedtgpqfeflvaywrrpgeaehtv 180  
 QY 181 KVRSGGIPVHLETMPEGAAYCVKAQTFVKAIGXSAFSQTECVQGEAIPVLALFAF 240  
 DB 181 kmvrsggipvhletmpegaaycvkaqtfvkaigrsafsqtecvqgeaipvlalfaf 240  
 QY 241 VGFMLILVVPLFVWKMRRLLOYSCCPVVVLPDITKITSPOKLTISCREEDACATAM 300  
 DB 241 vgfmlilvvplfvwkmrrllqysccpvvlpdtkltinspqkliscreedacatavm 300  
 QY 301 SPEELLRAMIS 311  
 DB 301 speellrawis 311

RESULT 2

ID AAB44292 standard; Protein; 311 AA.

XX AAB44292;

XX 08-FEB-2001 (first entry)

XX Human PRO1114 (UNQ557) protein sequence SEQ ID NO:352.

XX Human; secreted protein; transmembrane protein; PRO; EST; cytosolic;  
 KW expressed sequence tag; detection; cancer.

```
XX OS Homo sapiens.
XX PN WO200053756-A2.
XX PD 14-SEP-2000.
XX PF 18-FEB-2000; 2000WO-US04341.
XX PR 08-MAR-1999; 99WO-US05028.
PR 12-MAR-1999; 99US-0123957.
PR 29-MAR-1999; 99US-0126773.
PR 21-APR-1999; 99US-0130232.
PR 28-APR-1999; 99US-0131445.
PR 14-MAY-1999; 99US-0134287.
PR 23-JUN-1999; 99US-0141037.
PR 26-JUL-1999; 99US-0145698.
PR 29-OCT-1999; 99US-0162506.
PR 30-NOV-1999; 99WO-US28313.
PR 02-DEC-1999; 99WO-US28551.
PR 02-DEC-1999; 99WO-US28565.
PR 16-DEC-1999; 99WO-US30095.
PR 30-DEC-1999; 99WO-US31243.
PR 30-DEC-1999; 99WO-US31274.
PR 05-JAN-2000; 2000WO-US00219.
PR 06-JAN-2000; 2000WO-US00277.
XX PR 06-JAN-2000; 2000WO-US00376.
XX PA (GENE ) GENENTECH INC.
XX PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Fliviaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
PI Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;
PI Jhavan RJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA;
PI Shelton DL, Stewart TA, Tumas D, Williams PM, Wood WT;
XX DR MPI; 2000-611443/58.
XX DR N-PSDB; AAC78547.
XX PT Novel PRO polypeptides and polynucleotides used in detection methods,
XX PT to target bioactive molecules to specific cells, and to modulate
XX PT cellular activities -
XX PS Claim 12; Fig 142; 636pp; English.
XX CC AAC78458 to AAC78599 represent polynucleotide and EST (expressed
XX CC sequence tag) sequences which encode secreted or transmembrane PRO
XX CC polypeptides. The PRO polynucleotides and polypeptides have cytostatic
XX CC activity. The polynucleotides and polypeptides can be used for detecting
XX CC the presence of PRO polypeptides in samples, for linking bioactive
XX CC molecules to cells and for modulating biological activities of cells,
XX CC using the polypeptides for specific targeting. The polypeptide targeting
XX CC can be used to kill the target cells, e.g. for the treatment of cancers.
XX CC The polypeptide pairs provide specific targeting of bioactive molecules
XX CC to cells. AAC78600 to AAC78987 represent PCR primers and probes used in
XX CC the isolation of the PRO polynucleotide sequences.
XX SQ Sequence 311 AA:

Query Match 99.6%; Score 1620; DB 21; Length 311;
Best Local Similarity 98.7%; Pred. No. 6.5e-164;
Matches 307; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 MGTFTNVLLEIWTSLFMWFFALIPCLLTDEVALIPAPONTSVLSTNNKHLMSPVYAP 60
DB 1 mgtftmvlleewtslflmwfyalipclltdevallpapnslvstnnkhlmsvpylap 60
OY 61 GETVYVVEYGEYEGESLYTSHIMIPSSKCSLTGEGBCDYTDITATVYVNLNVRATLSQ 120
DB 61 getvyvveygeyegeslytshimipsscsltgegbcvtditativynlvratlsq 120
OY 121 TSAWSILKHPNRNSTILTRGMEIKKXGFLVLELEDLGQFERLVAVYKREPAEEHV 180
DB 121 TSAWSILKHPNRNSTILTRGMEIKKXGFLVLELEDLGQFERLVAVYKREPAEEHV 180
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DB 121 tsawsilknprnstilttrgmeltkdgflvleledlgqferlvayvrtpgaeehv 180
OY 181 KWRSGGIPVHLEETMEPGAAYCAVKAQTFVKAIXYSAFSGTECEVYOGGEAIPVLALFAF 240
DB 181 kwrsggipvhlleetmepgaaycvaqtfvkaigrasfsfgecevygegeaipvlalfaf 240
OY 241 VGFMLILVVPVLFVWKMGRLLOYSCCPVYVLPDTLKITNSPOKLISCRREEDACATAYM 300
DB 241 vgfmlilvvplfvwmkgrrlloysccpvvylpdtlkitnspoklisrreedacataym 300
OY 301 SPEELLRAWIS 311
DB 301 speellrawis 311

RESULT 3
AAB33440
ID AAB33440 standard; Protein; 311 AA.
XX AAB33440;
AC 29-JAN-2001 (first entry)
XX DT
XX DE Human PRO1114 protein UNQ557 SEQ ID NO:144.
XX XX
XX KW Human; immune related disease; diagnosis; antinflammatory; cardiant;
KW dermatological; antilarthritic; antirheumatic; immunosuppressive;
KW haemostatic; antithyroid; antidiabetic; neurotropic; neuroprotective;
KW antianaemic; hepatotropic; virucide; antiparasitic; antiallergic;
KW osteoarthritis; systemic lupus erythematosus; rheumatoid arthritis;
KW idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis;
KW systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus;
KW autoimmune thrombocytopenia; immune-mediated renal disease;
KW demyelinating disease; hepatobiliary disease; Whipple's disease;
KW inflammatory bowel disease; gluten-sensitive enteropathy;
KW autoimmune disease; immune-mediated skin disease; allergic disease;
KW immunological disease; transplantation associated disease;
KW graft rejection; graft-versus-host-disease.
XX OS Homo sapiens.
XX PN WO200053758-A2.
XX PD 14-SEP-2000.
XX PF 02-MAR-2000; 2000WO-US05841.
XX PR 08-MAR-1999; 99WO-US05028.
XX PR 10-MAR-1999; 99US-0123618.
XX PR 12-MAR-1999; 99US-0123957.
XX PR 12-MAR-1999; 99US-0125775.
XX PR 12-APR-1999; 99US-0128849.
XX PR 20-APR-1999; 99WO-US08615.
XX PR 28-APR-1999; 99US-0131445.
XX PR 04-MAY-1999; 99US-0132371.
XX PR 14-MAY-1999; 99US-0134287.
XX PR 02-JUN-1999; 99WO-US12252.
XX PR 23-JUN-1999; 99US-0141037.
XX PR 20-JUL-1999; 99US-0144758.
XX PR 26-JUL-1999; 99US-0145698.
XX PR 28-JUL-1999; 99US-0146222.
XX PR 01-SEP-1999; 99WO-US20111.
XX PR 08-SEP-1999; 99WO-US20594.
XX PR 13-SEP-1999; 99WO-US20944.
XX PR 15-SEP-1999; 99WO-US21540.
XX PR 15-SEP-1999; 99WO-US21597.
XX PR 05-OCT-1999; 99WO-US23089.
XX PR 29-OCT-1999; 99US-0162506.
XX PR 29-NOV-1999; 99WO-US28214.
XX PR 30-NOV-1999; 99WO-US28313.
XX PR 30-NOV-1999; 99WO-US28409.
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PR 01-DEC-1999: 99WO-US28301.  
 PR 01-DEC-1999: 99WO-US28634.  
 PR 02-DEC-1999: 99WO-US28551.  
 PR 02-DEC-1999: 99WO-US28565.  
 PR 02-DEC-1999: 99WO-US28565.  
 PR 16-DEC-1999: 99WO-US30095.  
 PR 20-DEC-1999: 99WO-US30989.  
 PR 30-DEC-1999: 99WO-US31274.  
 PR 05-JAN-2000: 2000WO-US00219.  
 PR 06-JAN-2000: 2000WO-US00277.  
 PR 06-JAN-2000: 2000WO-US00376.  
 PR 11-FEB-2000: 2000WO-US03565.  
 PR 18-FEB-2000: 2000WO-US04341.  
 PR 18-FEB-2000: 2000WO-US04342.  
 PR 22-FEB-2000: 2000WO-US04414.  
 (GENE ) GENENTECH INC.  
 Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W, Kabakoff RC, Lu Y, Pan J, Pennica D, Shelton DL, Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Yan M; WPI: 2000-572271/53.  
 N-PSDB: AAC58605.  
 Sixty four PRO polypeptides, useful in the diagnosis and treatment of immune related disorders, e.g. systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, thyroiditis and diabetes mellitus -  
 Claim 33; Fig 54; 309pp; English.  
 The present invention describes sixty four human PRO proteins which can be used in the treatment of immune related diseases. The human PRO proteins, anti-PRO antibodies, agonists and antagonists are useful for treating and diagnosing immune related disorders. The disorders are selected from systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, spondyloarthropathies, systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, demyelinating diseases of the central and peripheral nervous systems, hepatobiliary diseases, inflammatory bowel disease, gluten-sensitive enteropathy and Whipple's disease, autoimmune or immune-mediated skin diseases, allergic diseases, immunological diseases of the lung, and transplantation associated diseases including graft rejection and graft-versus-host-disease. AAC58397 to AAC58578 represent PCR primers and hybridisation probes used in the isolation of human PRO sequences. AAC58579 to AAC58642 and AAB33414 to AAB33477 represent human PRO polynucleotide and protein sequences given in the exemplification of the present invention.  
 Sequence 311 AA:  
 Query Match 99.6%; Score 1620; DB 21; Length 311;  
 Best Local Similarity 98.7%; Pred. No. 6.5e-164;  
 Matches 307; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 OY 1 MOFTVLEIEITSLFWMFYALIPCLITDEVAILPAPONLSVSTMKHLMSPIYAP 60  
 DB 1 mqfImvleieIwslImwIfyalIpclITdevalIpapqnlsvstmkhlmspyIap 60  
 OY 61 GETVYVSVEYGESELYTSYSHIMIPSSWCSLTGEGPECDVDDITATVPYNLRVATGSGQ 120  
 DB 61 geTvYvsveYgeSeLytsYshImIpssWcsLTgeGpeCDvDDITatVPynLRvatGsq 120  
 OY 121 TSAMSLIKAPFNNSSTILTRPGMEIKKXGFLVYLEDLAPQGEFFLVAYKXREPGEAHV 180  
 DB 121 tsamSlIkApfNnsStIltrPgMeIKKxGflVyleDLapQgeFFlVAyKxRePgeAhv 180  
 OY 181 KMWRSRGIRPHLEMTMGAAYCYKAGTFVAIGYSAFSOTECYEVGGEALPLVLAFAF 240  
 DB 181 kmwrsrgIrPhleMTmGaAYcYkAGtFvAIGySAfSOTeCYeVgGeAlPlVlAfaF 240

OY 241 VGFMLILVVPLEFWKMGRLQYSCCPVVVLPDTEKITSNPQKLISCRREVDACATAVM 300  
 DB 241 vgfmlilvvpLefwKmgRLqYscCPvvVlpDteKItSNpQklIScrReVdaCaTavM 300  
 OY 301 SPEELLRAWIS 311  
 DB 301 speellrawis 311  
 RESULT 4  
 ID AAY97046 standard; Protein: 311 AA.  
 AC AAY97046;  
 XX 31-OCR-2000 (first entry)  
 DE Human TANGO 242.  
 XX TANGO 242; transmembrane; class II; cytokine receptor; chromosome 3q21;  
 KW cytosolic; cerebroprotective; immunomodulatory; anti-inflammatory;  
 KW virucide; antibacterial; vasotropic.  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..29  
 FT Protein /label= Signal\_peptide 30..311  
 FT Domain /label= Mature\_protein 30..230  
 FT Modified-site /label= Extracellular\_domain 40  
 FT /note= "N-linked glycosylation site" 35..125  
 FT /label= Fibronectin\_III\_domain 134  
 FT Modified-site /note= "N-linked glycosylation site" 231..255  
 FT /label= Transmembrane\_domain 256..311  
 FT Domain /label= Cytoplasmic\_domain  
 XX  
 PN WO200039161-A1.  
 XX 06-JUL-2000.  
 XX 30-DEC-1999; 99WO-US31328.  
 XX 31-DEC-1998; 98US-0224669.  
 PA (MILL-) MILLENNIUM PHARM INC.  
 XX  
 PI Busfield SJ;  
 PI WPI: 2000-452372/39.  
 DR N-PSDB: AAA51871, AAA51872.  
 XX New nucleic acid molecules encoding polypeptides designated TANGO 241 and TANGO 242 used for treating e.g. brain and pancreatic disorders  
 PS Claim 8; Fig 3; 127pp; English.  
 XX Novel transmembrane proteins, designated TANGO 241 and TANGO 242, are members of the class II cytokine receptor superfamily. The TANGO 241 and 242 genes have been localized to human chromosomes 1p36 and 3q21, respectively. The proteins, cDNA and their modulators can be used for the treatment of viral and bacterial infection, inflammatory and autoimmune disorders, vascular injury and inhibition of angiogenesis. In particular, TANGO 241 can be used to treat pancreatic disorders and TANGO 242 can be used to treat brain disorders.



OS Homo sapiens.  
 XX WO9963088-A2.  
 PN  
 XX  
 PD 09-DEC-1999.  
 XX  
 PF 02-JUN-1999; 99WO-US12252.  
 XX  
 PR 02-JUN-1998; 98US-0087607.  
 PR 02-JUN-1998; 98US-0087609.  
 PR 02-JUN-1998; 98US-0087759.  
 PR 03-JUN-1998; 98US-0087827.  
 PR 04-JUN-1998; 98US-0088021.  
 PR 04-JUN-1998; 98US-0088025.  
 PR 04-JUN-1998; 98US-0088028.  
 PR 04-JUN-1998; 98US-0088029.  
 PR 04-JUN-1998; 98US-0088030.  
 PR 04-JUN-1998; 98US-0088033.  
 PR 04-JUN-1998; 98US-0088326.  
 PR 05-JUN-1998; 98US-0088167.  
 PR 05-JUN-1998; 98US-0088202.  
 PR 05-JUN-1998; 98US-0088212.  
 PR 05-JUN-1998; 98US-0088217.  
 PR 09-JUN-1998; 98US-0088655.  
 PR 10-JUN-1998; 98US-0088722.  
 PR 10-JUN-1998; 98US-0088730.  
 PR 10-JUN-1998; 98US-0088734.  
 PR 10-JUN-1998; 98US-0088738.  
 PR 10-JUN-1998; 98US-0088740.  
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 PR 10-JUN-1998; 98US-0088742.  
 PR 10-JUN-1998; 98US-0088810.  
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 PR 10-JUN-1998; 98US-0088824.  
 PR 10-JUN-1998; 98US-0088825.  
 PR 11-JUN-1998; 98US-0088826.  
 PR 11-JUN-1998; 98US-0088858.  
 PR 11-JUN-1998; 98US-0088861.  
 PR 11-JUN-1998; 98US-0088863.  
 PR 11-JUN-1998; 98US-0088876.  
 PR 12-JUN-1998; 98US-0088909.  
 PR 12-JUN-1998; 98US-0089105.  
 PR 16-JUN-1998; 98US-0089440.  
 PR 16-JUN-1998; 98US-0089512.  
 PR 16-JUN-1998; 98US-0089514.  
 PR 17-JUN-1998; 98US-0089532.  
 PR 17-JUN-1998; 98US-0089538.  
 PR 17-JUN-1998; 98US-0089598.  
 PR 17-JUN-1998; 98US-0089599.  
 PR 17-JUN-1998; 98US-0089600.  
 PR 17-JUN-1998; 98US-0089653.  
 PR 18-JUN-1998; 98US-0089801.  
 PR 18-JUN-1998; 98US-0089907.  
 PR 18-JUN-1998; 98US-0089908.  
 PR 19-JUN-1998; 98US-0089947.  
 PR 19-JUN-1998; 98US-0089948.  
 PR 19-JUN-1998; 98US-0089952.  
 PR 22-JUN-1998; 98US-0090246.  
 PR 22-JUN-1998; 98US-0090252.  
 PR 22-JUN-1998; 98US-0090254.  
 PR 23-JUN-1998; 98US-0090349.  
 PR 23-JUN-1998; 98US-0090355.  
 PR 24-JUN-1998; 98US-0090429.  
 PR 24-JUN-1998; 98US-0090431.  
 PR 24-JUN-1998; 98US-0090435.  
 PR 24-JUN-1998; 98US-0090444.  
 PR 24-JUN-1998; 98US-0090445.  
 PR 24-JUN-1998; 98US-0090461.  
 PR 24-JUN-1998; 98US-0090472.  
 PR 24-JUN-1998; 98US-0090535.  
 PR 24-JUN-1998; 98US-0090538.  
 PR 24-JUN-1998; 98US-0090540.  
 PR 24-JUN-1998; 98US-0090557.

PR 25-JUN-1998; 98US-0090676.  
 PR 25-JUN-1998; 98US-0090678.  
 PR 25-JUN-1998; 98US-0090688.  
 PR 25-JUN-1998; 98US-0090690.  
 PR 25-JUN-1998; 98US-0090691.  
 PR 25-JUN-1998; 98US-0090694.  
 PR 25-JUN-1998; 98US-0090695.  
 PR 25-JUN-1998; 98US-0090696.  
 PR 26-JUN-1998; 98US-0090697.  
 PR 26-JUN-1998; 98US-0090698.  
 PR 01-JUL-1998; 98US-0091358.  
 PR 01-JUL-1998; 98US-0091360.  
 PR 01-JUL-1998; 98US-0091364.  
 PR 02-JUL-1998; 98US-0091478.  
 PR 02-JUL-1998; 98US-0091486.  
 PR 02-JUL-1998; 98US-0091519.  
 PR 02-JUL-1998; 98US-0091626.  
 PR 02-JUL-1998; 98US-0091628.  
 PR 02-JUL-1998; 98US-0091633.  
 PR 02-JUL-1998; 98US-0091646.  
 PR 02-JUL-1998; 98US-0091673.  
 PR 07-JUL-1998; 98US-0091678.  
 PR 07-JUL-1998; 98US-0091982.  
 PR 09-JUL-1998; 98US-0092182.  
 PR 10-JUL-1998; 98US-0092472.  
 PR 20-JUL-1998; 98US-0093339.  
 PR 30-JUL-1998; 98US-0094651.  
 PR 04-AUG-1998; 98US-0095282.  
 PR 04-AUG-1998; 98US-0095285.  
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 PR 04-AUG-1998; 98US-0095318.  
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 PR 10-AUG-1998; 98US-0095916.  
 PR 10-AUG-1998; 98US-0095929.  
 PR 10-AUG-1998; 98US-0096012.  
 PR 11-AUG-1998; 98US-0096143.  
 PR 11-AUG-1998; 98US-0096146.  
 PR 12-AUG-1998; 98US-0096329.  
 PR 17-AUG-1998; 98US-0096757.  
 PR 17-AUG-1998; 98US-0096766.  
 PR 17-AUG-1998; 98US-0096768.  
 PR 17-AUG-1998; 98US-0096773.  
 PR 17-AUG-1998; 98US-0096791.  
 PR 17-AUG-1998; 98US-0096867.  
 PR 17-AUG-1998; 98US-0096891.  
 PR 17-AUG-1998; 98US-0096894.  
 PR 17-AUG-1998; 98US-0096895.  
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 PR 18-AUG-1998; 98US-0096949.  
 PR 18-AUG-1998; 98US-0096950.  
 PR 18-AUG-1998; 98US-0096959.  
 PR 18-AUG-1998; 98US-0096960.  
 PR 18-AUG-1998; 98US-0096966.  
 PR 18-AUG-1998; 98US-0097022.  
 PR 19-AUG-1998; 98US-0097141.  
 PR 20-AUG-1998; 98US-0097218.  
 PR 24-AUG-1998; 98US-0097661.  
 PR 26-AUG-1998; 98US-0097951.  
 PR 26-AUG-1998; 98US-0097952.  
 PR 26-AUG-1998; 98US-0097954.  
 PR 26-AUG-1998; 98US-0097955.  
 PR 26-AUG-1998; 98US-0097971.  
 PR 26-AUG-1998; 98US-0097974.  
 PR 26-AUG-1998; 98US-0097978.  
 PR 26-AUG-1998; 98US-0097979.  
 PR 26-AUG-1998; 98US-0097986.  
 PR 26-AUG-1998; 98US-0098014.  
 PR 31-AUG-1998; 98US-0098525.  
 PR 16-SEP-1998; 98US-0100634.  
 PR 12-JAN-1999; 99US-0115565.  
 XX  
 PA (GETH ) GENENTECH INC.

Query Match	Best Local Similarity	98.7%	Score 1620;	DB 21;	Length 311;
Matches	307;	Conservative	0;	Mismatches	4;
				Indels	0;
				Gaps	0
QY 1	MOTFMVLEELTSLPMMFEVALLPCLLTDEVAIIIPAPONLSVLTNKHLMMSVYIAP	60			
DB 1	mqftmfvleelvtstslfmwffiyallpcollddevaillpapqnlsvlstrnmkhllmwspsviap	60			
QY 61	GETVYVSYVEYQGEYSILVYSHTWISSWCSLREGPCVDVTDITAVPYNLKVRAVLGSO	120			
DB 61	getvysveyqgeysilvshwipsswsclslegpcdvlditavpynlvtvratlgseq	120			
QY 121	TSAMSLKHPPFRNRSTIIILRPGMEILKXKGFHLVIELEDGDPQFEFLVAVWXRPGAEHHY	180			
DB 121	tsawslkhppfrnrstiiilrpgmeltkgfhlvleledlgpqfeflvaywrrpgaeehy	180			
QY 181	KWNRSGGIPVHLETPMGCAVCVKAQTEVKAIGXYSAFSQTECEVQGAIPLVIALFAF	240			
DB 181	kwivsggipvhletemepgacvckaqtfkaiqrgysafsqteceveqgaipvlialfaf	240			
QY 241	VEFMILIVVPLPFWKMGRLLOYSCPPVVLRBDTLKITNSPQKLISGREEDVACTATAM	300			
DB 241	vqfmilivvplpflwkmgrllqysccpvpvlpdcltkltnspklliscreevadacataam	300			
QY 301	SPEELLRAWIS 311				
DB 301	speellrawis 311				
RESULT 7					
ID AAB65199	standard; Protein; 311 AA.				
XX AAB65199;					
DT 02-APR-2001	(first entry)				
XX Human PRO1114	(UNQ557) protein sequence SEQ ID NO:183.				
XX Human; secreted and transmembrane protein; PRO; cytosolic;					
KW cell death; cancer; chromosomal mapping; gene mapping; tissue typing;					
XX diagnostic assay.					
XX Homo sapiens.					

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XX PN WO200073454-A1.
XX PD
XX 07-DEC-2000.
XX PF
XX 30-MAR-2000; 2000OWO-US08439.
XX
PR 02-JUN-1999; 99WO-US12252.
PR 23-JUN-1999; 99US-0141037.
PR 07-JUL-1999; 99US-0143048.
PR 20-JUL-1999; 99US-0144758.
PR 26-JUL-1999; 99US-0145698.
PR 28-JUL-1999; 99US-0146222.
PR 17-AUG-1999; 99US-0149366.
PR 15-SEP-1999; 99WO-US21090.
PR 15-SEP-1999; 99WO-US21547.
PR 08-OCT-1999; 99US-0158663.
PR 30-NOV-1999; 99WO-US28313.
PR 01-DEC-1999; 99WO-US28301.
PR 16-DEC-1999; 99WO-US30095.
PR 20-DEC-1999; 99WO-US30911.
PR 05-JAN-2000; 2000OWO-US00219.
PR 06-JAN-2000; 2000OWO-US00376.
PR 11-FEB-2000; 2000OWO-US03565.
PR 18-FEB-2000; 2000OWO-US04341.
PR 22-FEB-2000; 2000OWO-US04414.
PR 24-FEB-2000; 2000OWO-US04914.
PR 24-FEB-2000; 2000OWO-US05004.
PR 02-MAR-2000; 2000OWO-US05841.
PR 15-MAR-2000; 2000OWO-US06884.
PR 20-MAR-2000; 2000OWO-US07377.
XX
XX (GETH ) GENENTECH INC.
PA
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrera N, Fong S, Geber H, Gerlitsen ME, Goddard A, Godowski PJ;
PI Grimaldi CJ, Gunney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WT;
PI Zhang Z;
XX
XX WPI: 2001-032160/04.
DR N-PSDB; AAF44157.
XX
PT PRO polynucleotides used to produce polypeptides used to target
PT bioactive molecules such as toxins, radiolabels or antibodies, to
PT specific cells, to cause targeted cell death -
XX
PS Claim 12; Fig 117; 935pp; English.
XX
CC The present invention describes human secreted and transmembrane PRO
CC proteins. The PRO proteins have cytosstatic activity. The PRO proteins
CC can be used for targeted delivery of bioactive molecules, such as
CC toxins, radiolabels or antibodies, that cause cell death. PRO nucleotide
CC sequences, and their fragments, can be used as hybridisation probes, in
CC chromosomal and gene mapping, and in the generation of anti-sense RNA
CC and DNA. They may also be used to produce transgenic animals which are
CC used to develop and screen therapeutically useful reagents. The PRO
CC nucleotide and protein sequence can be used for tissue typing and in
CC treating cancer. Anti-PRO antibodies can be used in diagnostic assays.
CC AAF44270 to AAF44470 represent PCR primers and hybridisation probes used
CC in the isolation of human PRO sequences. AAF44087 to AAF44269 and
CC AAB65154 to AAB65300 represent human PRO polynucleotide and protein
CC sequences given in the exemplification of the present invention.
XX
XX Sequence 311 AA:
SQ
Query Match 99.6%; Score 1620; DB 22; Length 311;
Best Local Similarity 98.7%; Pred. No. 6,5e-16;
Matches 307; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
1 MGFNNVLEIWTSLFMFFVALLICLLTDEVAIIIPAPONLSVLSTNNKHLMMSPVIAP 60
|||||

```



```

Db      1 mqlftmveeiwtslfmwffiyalipclltdevallpapqnlsvlstmkhllmwsplap 60
QY      61 GETVYVSVEYGGESLYTSHTIMIPSSWCSLTGEGPCDVTDDITATVPYNLRVRATLGSQ 120
        |||
Db      61 getvyvsveyggeslytshtlwpsswcsltegpedcvdditativynlrvratlgsq 120
QY      121 TSAMSLIKHPENRSTILTRPGMEIKKXGPHLYIELEDLGPQEFELVAYXKREGAEHV 180
        |||
Db      121 tsawslkhphnrstlitrpgmekdghlyleledlqpqfeflvayvrrepgaehev 180
QY      181 KMWRSGLIPVHLETMEPGAAVCYKAQTFVKAIGXSAFSQTECEVGGELIPVLALFAF 240
        |||
Db      181 kmvrsqgipvhletmepgaaycvkaqtfvkaigrsafsqtecevggeaipvlalfaf 240
QY      241 VGFMLILVVPPLFWKMGRLQYSCCPVYVLPDTLKITNSPORKLISCRREVDACATAVM 300
        |||
Db      241 vgfmlilvvpplfwkmgrllyscpcpvvlpdtlkitnspqklisrreevdacatavm 300
        |||
        301 SPEELLRAWIS 311
        |||
        301 speellrawis 311

```

## RESULT 8

AA939472 ID AAY39472 standard; Protein; 311 AA.

AC AAY39472;

DT 19-NOV-1999 (first entry)

DE DNAX Interferon-like receptor subunit 1 protein sequence.

KM DNAX interferon-like receptor subunit; DIRS1; DIRS2; cytokine receptor; therapy; degenerative condition; abnormal condition; cellular development; cell differentiation.

OS Homo sapiens.

PN WO9946379-A2.

PD 16-SEP-1999.

PF 08-MAR-1999; 99WO-US03735.

PR 09-MAR-1998; 98US-0037394.

XX (SCHE) SCHERING CORP.

PI Parham CL, Moore KW, Murgolo NJ, Bazan JF;

DR WPI; 1999-551408/46.

DR N-PSDB; AA20504.

PT New receptor subunits potentially useful, e.g. for treating degenerative and abnormal conditions that involve cellular development,

PS Claim 1; Page 74-76; 82pp; English.

CC This sequence is the DNAX Interferon-like receptor subunit 1 (DIRS1) of the invention. The invention also relates to the DIRS2 protein sequence. The DIRS1 and DIRS2 sequences are subunits of receptors related to cytokine receptors. The isolated receptor gene provides means to generate an economical source of the receptor, allow expression of more receptors on a cell leading to increased assay sensitivity, promote characterization of various receptor subtypes and variants, and allow correlation of activity with receptor structures. The invention should contribute to new therapies for degenerative and abnormal conditions that involve cellular development, differentiation or function.

XX Sequence 311 AA.

Query Match 99.5%; Score 1619; DB 20; Length 311;  
 Best Local Similarity 98.7%; Pred. No. 8.3e-164;  
 Matches 307; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```

QY      1 MQFTMVEEITSLFMWFFIYALIPCLLTDEVALIPAPQNLVSTNMKHLIMWSPLAP 60
        |||
Db      1 mqlftmveeiwtslfmwffiyalipclltdevallpapqnlsvlstmkhllmwsplap 60
QY      61 GETVYVSVEYGGESLYTSHTIMIPSSWCSLTGEGPCDVTDDITATVPYNLRVRATLGSQ 120
        |||
Db      61 getvyvsveyggeslytshtlwpsswcsltegpedcvdditativynlrvratlgsq 120
QY      121 TSAMSLIKHPENRSTILTRPGMEIKKXGPHLYIELEDLGPQEFELVAYXKREGAEHV 180
        |||
Db      121 tsawslkhphnrstlitrpgmekdghlyleledlqpqfeflvayvrrepgaehev 180
QY      181 KMWRSGLIPVHLETMEPGAAVCYKAQTFVKAIGXSAFSQTECEVGGELIPVLALFAF 240
        |||
Db      181 kmvrsqgipvhletmepgaaycvkaqtfvkaigrsafsqtecevggeaipvlalfaf 240
QY      241 VGFMLILVVPPLFWKMGRLQYSCCPVYVLPDTLKITNSPORKLISCRREVDACATAVM 300
        |||
Db      241 vgfmlilvvpplfwkmgrllyscpcpvvlpdtlkitnspqklisrreevdacatavm 300
QY      301 SPEELLRAWIS 311
        |||
Db      301 speellrawis 311

```

## RESULT 9

AA97048 ID AAY97048 standard; Protein; 308 AA.

AC AAY97048;

DT 31-OCT-2000 (first entry)

DE Murine TANGO 242.

KM TANGO 242; transmembrane; class II; cytokine receptor; cytostatic; cerebroprotective; immunomodulatory; anti-inflammatory; virocidic;

KW antibacterial; vasotropic.

OS Mus sp.

PN WO200039161-A1.

PD 06-JUL-2000.

PF 30-DEC-1999; 99WO-US31328.

PR 31-DEC-1998; 98US-0224669.

PA (MILL-) MILLENNIUM PHARM INC.

PI Busfield SJ;

DR WPI; 2000-452372/39.

DR N-PSDB; AAA51875, AAA51876.

PT New nucleic acid molecules encoding polypeptides designated TANGO 241 and TANGO 242 used for treating e.g. brain and pancreatic disorders

PS Disclosure; Fig 8A-B; 127pp; English.

CC Novel transmembrane proteins, designated TANGO 241 and TANGO 242, are members of the class II cytokine receptor superfamily. The TANGO 241 and 242 genes have been localized to human chromosomes 1p36 and 3q21, respectively. The proteins, cDNA and their modulators can be used for the treatment of viral and bacterial infection, inflammatory and autoimmune disorders, vascular injury and inhibition of angiogenesis. In particular, TANGO 241 can be used to treat pancreatic disorders and TANGO 242 can be

CC used to treat brain disorders.  
 XX  
 SQ Sequence 308 AA:

Query Match 76.4%; Score 1243; DB 21; Length 308;  
 Best Local Similarity 76.5%; Pred. No. 7,8e-124;  
 Matches 234; Conservative 24; Mismatches 48; Indels 0; Gaps 0;

6 MLEETWISLPMFAYALPCLITDEVALIPAPONSVLSTNKHLLMSPVIAPEYV 65  
 1 mlsqgvwtselpimwffysmcsfltdavsvlpapqnlsvstmxkhllmnpvqpeyvl 60  
 66 YSVEYOGESLYTSHIWPSSWCSLTGEPEDVDITATVPYNLRVRAITLGSQTSAMS 125  
 61 YVEYVGEYESLYMSHIWPSSWCSLTGEPEDVDITATVPYNLRVRAITLGSQTSAMS 120  
 126 ILKHFPNRSTLITRGMILKXGFLHYLEDELGQFELVAKYKREPAEHHVMKRS 185  
 121 nlehpfnratvltprmevntehghlvleledl9pqfelfvvywrtrepgaaehvkmvrs 180  
 186 GIPHLEMEPGAACVKAQTFVKAIGKXSAFSQTECEVOGEALPLVLAFAFGFML 245  
 181 gdlphletemeganycvagatvkaigthsatsqptcemggeslplatafatygm 240  
 246 ILVVVPLEFMKGRLLQYSCCPVYVLPDLTKITNSPOKLISCRREEVDAATVMSPEEL 305  
 241 ilvvvllsvwmqgllrlyscpavvlpdltkltsesqkliscrkeevdaavavlseshl 300  
 306 LRAMIS 311  
 301 fgvwis 306

## RESULT 10

AAG03609  
 ID AAG03609 standard; Protein; 100 AA.

AC AAG03609;

DT 06-OCT-2000 (first entry)

DE Human secreted protein, SEQ ID NO: 7690.

KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;

KV gene therapy; chromosome mapping.

OS Homo sapiens.

XX EP1033401-A2.

PD 06-SEP-2000.

PF 21-FEB-2000; 2000EP-0200610.

PR 26-FEB-1999; 99US-0122487.

PA (GEST ) GENSET.

PI Dumas Milne Edwards J, Duclert A, Giordano J;

DR WPI; 2000-500381/45.

DR N-PSDB; AAC03615.

XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for  
 PT obtaining cDNAs and genomic DNAs that correspond to 5' ESTs and for  
 PT diagnostic, forensic, gene therapy and chromosome mapping procedures -  
 XX Claim 13; SEQ ID 7690; 71pp + CD-ROM; English.

XX The present sequence is a polypeptide encoded by one of a large number  
 CC of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs  
 CC were prepared from total human RNAs or polyA+ RNAs derived from 30

CC different tissues. EST sequences usually correspond mainly to the 3'  
 CC untranslated region (UTR) of the mRNA because they are often obtained  
 CC from oligo-dT primed cDNA libraries. Such ESTs are not well suited for  
 CC isolating cDNA sequences derived from the 5' ends of mRNAs and even in  
 CC those cases where longer cDNA sequences have been obtained, the full 5'  
 CC UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5'  
 CC ends and can therefore be used to obtain full length cDNAs and genomic  
 CC DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and  
 CC chromosome mapping procedures. They are used to obtain upstream  
 CC regulatory sequences and to design expression and secretion vectors.  
 XX  
 SQ Sequence 100 AA:

Query Match 32.5%; Score 529; DB 21; Length 100;  
 Best Local Similarity 98.0%; Pred. No. 1.3e-48;  
 Matches 98; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MGFYVLEETWISLPMFAYALPCLITDEVALIPAPONSVLSTNKHLLMSPVIAPE 60  
 1 mgtflwleelwtslpmfayalpxlltdevallpapqnlsvstmxkhllmwpviap 60  
 61 GEPYYSVEYOGESLYTSHIWPSSWCSLTGEPEDVT 100  
 61 getvyysveyqgeyeslytshiwipswcsltgepedvt 100

## RESULT 11

AAM52296  
 ID AAM52296 standard; Protein; 325 AA.

AC AAM52296;

DT 23-JUN-1998 (first entry)

DE CRFB4 protein.

KW CRFB4; interleukin-10; IL-10; IL-10 receptor; allograft rejection;

KV vaccine; photosensitivity; inflammation; autoimmune disease;

KW septic shock; immune response; organ rejection; gene therapy.

OS Homo sapiens.

PN MO9802542-A1.

PD 22-JAN-1998.

PF 17-JUL-1997; 97WO-US12455.

PR 17-JUL-1996; 96US-0683743.

PA (UYNE-) UNIV NEW JERSEY.

PI Kottenko SV, Pestka S;

DR WPI; 1998-110590/10.

DR N-PSDB; AAV19874.

XX New recombinant DNA - comprises sequences encoding interleukin-10  
 PT and CRFB4 linked to operator, useful, e.g. preventing allograft  
 PT rejection  
 XX Claim 2; Page -: 79pp; English.

XX This sequence is the human CRFB4 sequence, DNA encoding it is used in the  
 CC recombinant DNA (1) of the invention. (1) comprises a sequence (S1)  
 CC encoding the interleukin-10 (IL-10) receptor (IL10R) and a sequence (S2)  
 CC encoding CRFB4, both operably linked to expression control sequences.  
 CC Cells containing (1) may be used to identify agonists/antagonist of  
 CC IL-10. Agonists are potentially useful, e.g. for preventing allograft  
 CC rejection, as vaccine adjuvants, for treatment of photosensitivity,  
 CC inflammation, autoimmune disease and septic shock, while antagonists are  
 CC potentially useful for increasing immune responses against tumours,

CC viruses, bacteria and parasites (especially intracellular pathogens) and  
 CC for preventing organ rejection. A vector containing (1) is used to  
 CC restore, e.g. by gene therapy, IL-10 sensitivity to a cell that expresses  
 CC a dysfunctional IL10R and is able to bind IL-10 but not to transduce a  
 CC signal. Antisense CRF4 sequences (especially ribozymes), can inhibit  
 CC IL-10 activity in cells. Antibodies specific for CRF4 are used to  
 CC measure and localise CRF4, for diagnosis of defective IL-10 activity.  
 CC Fragments of (1) are used as primers or probes to assay CRF4-specific  
 CC RNA. Agonists/antagonists may be administered parenterally, orally or  
 CC rectally especially by intravenous injection or directly into a tumour or  
 CC allograft.

CC Sequence 325 AA;

Query Match 11.7%; Score 191; DB 19; Length 325;

Best Local Similarity 26.6%; Pred. No. 6,2e-12;

Matches 77; Conservative 47; Mismatches 117; Indels 48; Gaps 16;

12 WTSLEMFYALIPCLTDEVALIPAPONLSVLTSMKHLMM-SPVIAPEYVYSEY 70

3 W-sigsw----lgccllvsalgmwppenvrmasvnfknlqwesafakg-----nltf 52

71 QGEYSLYTSHIWPSSMCSITEGECDDVTDITATVPYNLRVATLGSQTSAM-SILKH 129

53 taqylsy-----lfqdkcmlltlecds-slskygdhltrvaefadshdwntlfc 106

130 PFNNSITLTPGMEIKKXGFHLVLEEDLGPQFE-----FLVAYMXRE 173

107 pv--dtilppmqvveladsl--hmfllapkleneyetlmknyvswyngyw--k 160

174 PGAEHVKWVRSGIPVHLETPMGACVKAQGFVKAIGXYSFSGTECEV-VQGEAIP 232

161 ngtlekfgitpdyqfev-lrnlepwtcyvgrglpdrnkagsevpceqtlthdelpv 219

233 ---LVLLAFVGFMLIVVPLF--VWKGRLQYSCCPVVLPTDK 276

220 smwaavilmasv-fmvcallgctslwcykktkylatsprnsipqnlk 267

RESULT 12

AAB31214

AAB31214 standard; Protein: 325 AA.

AC

20-APR-2001 (first entry)

Amino acid sequence of human polypeptide PRO2630.

Human; secreted protein; transmembrane protein; PRO196; PRO444; PRO183;

PRO185; PRO210; PRO215; PRO217; PRO242; PRO288; PRO365; PRO1361; PRO1308;

PRO1183; PRO1272; PRO1419; PRO4999; PRO1710; PRO248; PRO353; PRO1318;

PRO1600; PRO3940; PRO333; PRO301; PRO187; PRO337; PRO1411; PRO4356;

PRO246; PRO365; PRO941; PRO10096; PRO6003; PRO6004; PRO350; PRO2630;

PRO6309; cell death; genetic disorder; transgenic animal; gene therapy.

XX Homo sapiens.

XX

XX

XX

XX

XX

XX

XX

XX

FT Domain /note= "N-glycosylation site"  
 FT 222..245  
 FT /note= "transmembrane domain"  
 FT Modified-site 316..322  
 FT /note= "N-myristoylation site"

WO200077037-A2.

21-DEC-2000.

22-MAY-2000; 2000WO-US14042.

15-JUN-1999; 99US-0139695.

20-JUL-1999; 99US-0145070.

26-JUL-1999; 99US-0145698.

17-AUG-1999; 99US-0149396.

01-SEP-1999; 99WO-US20111.

08-SEP-1999; 99WO-US20594.

15-SEP-1999; 99WO-US21090.

30-NOV-1999; 99WO-US21547.

01-DEC-1999; 99WO-US28313.

02-DEC-1999; 99WO-US28301.

07-DEC-1999; 99US-0169495.

05-JAN-2000; 2000WO-US00219.

18-FEB-2000; 2000WO-US04341.

18-FEB-2000; 2000WO-US04342.

22-FEB-2000; 2000WO-US04414.

01-MAR-2000; 2000WO-US05601.

02-MAR-2000; 2000WO-US05841.

20-MAR-2000; 2000WO-US07377.

30-MAR-2000; 2000WO-US08439.

15-MAY-2000; 2000WO-US13358.

17-MAY-2000; 2000WO-US13705.

(GENE ) GENENTECH INC.

Ashkenazi AJ, Baker KP, Bolstein DA, Desnoyers L, Eaton DL;

Ferrara N, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;

Godowski PJ, Gurney AJ, Kljavin IJ, Mather JP, Napier MA, Pan J;

Paoni NF, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PW;

Wood WJ, Zhang Z;

WPI: 2001-050091/06.

DR N-PSDB; AAC87060.

Isolated nucleic acid molecule encoding a PRO polypeptide which is a

transmembrane polypeptide is useful for gene therapy and identification

of related polypeptides -

Claim 12; Fig 72; 244pp; English.

The present sequence represents a human secreted and transmembrane

polypeptide. The specification describes human polypeptides, designated

PRO196, PRO444, PRO183, PRO210, PRO217, PRO242, PRO288,

PRO1361, PRO1308, PRO1183, PRO1272, PRO1419, PRO4999, PRO1710,

PRO248, PRO353, PRO1318, PRO1600, PRO9940, PRO533, PRO301, PRO187,

PRO337, PRO1411, PRO4356, PRO246, PRO265, PRO941, PRO10096, PRO6003,

PRO6004, PRO350, PRO2630 and PRO6309. The biological activity of cells

can be modulated with agents that bind to these polypeptides, resulting

in the death of the cells. The polynucleotides encoding these

polypeptides are useful in the recombinant production of the

polypeptides, as a hybridisation probe to screen libraries to isolate

homologous sequences, or to map the gene. They may also be used for

analysing genetic disorders, and to produce transgenic animals which are

useful for the development and screening of therapeutically useful

reagents. The polynucleotides can also be used in gene therapy e.g. to

replace a defective gene.

Sequence 325 AA;

Query Match 11.7%; Score 191; DB 22; Length 325;



```

QY 69 EYGEVESLTSIMWIPSSMCSLGEPCDVTDTITATP-----YMLRATIGS 119
Db 66 qfkytskwtadmsigvctgtatec-----dfiaapsagfpmfnnlrlraelga 121
QY 120 QTSAMSLT---KHPFNNSSTILFRPGMEIKKXGFHLVI-----ELDLGPQFE-PLVAY 169
Db 122 lhaawtumpvfgn-yrvntvgppenievprgegsllilrfspridactstafcyvhy 179
QY 170 WKREPGAEEHV-KVRSGGIPVHLETPMGAAYCVKAQ-----TFVKAIGXSAFSQT 221
Db 180 w--ekggigqvkqpfirsnsi--sldnlkpsrvcyqlqvgaqlmknknlffrvghlns-- 233
QY 222 ECEVGECEA-IPVLALFARVGFMLILVVP-----LFVWKMGRLQY 263
Db 234 -cydlnadaastelqvyllsvgtfllsvlagacflvlykryglyk 279

```

RESULT 15

28496 AAR28496 standard; Protein; 557 AA.

XX AAR28496;

DT 31-MAR-1993 (first entry)

DE Sequence of a soluble form of the interferon (IFN) receptor  
DE with a high affinity for IFN-alpha and -beta.

KM Interferon receptor; alpha-interferon; beta-interferon.

OS Synthetic.

XX W09218626-A.

PD 29-OCT-1992.

PF 17-APR-1991: 91MO-FR00318.

PR 17-APR-1991: 91MO-FR00318.

PA (EUBI-) LAB EURO BIOTECHNOLOGIE.

PI Eid P, Gresser I, Lutfalla G, Meyer F, Mogensen KE;

PI Tovey M, Uze G;

DR WPI; 1992-382110/46.

N-PSDB; AAQ30533.

PT Water soluble polypeptide(s) strongly bind interferon(s) alpha  
PT and beta - useful as immunosuppressants, for treating auto-immune  
PT diseases and transplant rejection

PS Claim 3; Fig 2; 58pp; English.

CC DNA encoding the water-soluble polypeptide with a high affinity for  
CC IFN-alpha and -beta is isolated by PCR, using appropriate  
CC oligonucleotides as primers and cloned cDNA as template. For example,  
CC bacteriophage lambda ZAP, containing the entire coding sequence of  
CC the IFN-alpha and -beta receptor (AAQ30533), was incubated with oligos  
CC AAQ30534 and AAQ30535. AAR28496 represents the complete receptor.  
CC AAR28495 lacks the transmembrane and cytoplasmic domains. Both forms  
CC bind IFN in the same way as antibodies so are immunosuppressants e.g.  
CC for treating autoimmune diseases and graft rejection. They lack the  
CC toxic side-effects of known immunosuppressants such as steroids.

XX Sequence 557 AA;

Query Match 10.0%; Score 163.5; DB 13; Length 557;  
Best Local Similarity 22.0%; Pred. No. 1.1e-08;  
Matches 71; Conservative 54; Mismatches 115; Indels 83; Gaps 17;

```

QY 21 YALIRCLTDEVAIIPAPQNLSTVSTNMKHLMSPIAPCTVYYSVEYGEYSLSLT- 79
Db 215 yspvhciktveenelpppenlevsvqngnylkw-----dytanmtfgyqwlhafik 267
QY 80 ---SHWIPSSMCSLGEPCDVTDTITATVPYN-----LFRATIGSQTAMS-- 125
Db 268 rnpqnily---kwkq1---pdceavkltqcvfpqnvfqkyllyllrvqasdgntsfwsee 321
QY 126 -----LKHPFNNSSTILFRPGMEIKKXGFHLVI-----ELDLGPQFEF 165
Db 322 ikfdeiqafllppvfnlrs-----lsdsfhiyigapkgsgnprvidqpllye- 370
QY 166 LVATWKRPGAEEHV-KVRSGGIPVHLETPMGAAYCVKAQ--TFVKAIGXSAFSQT 223
Db 371 -lftwentsnaerklietkt--dvtvpnlkpltycvkarahtmdexlnksvfsdave 426
QY 224 VEVO-GEAIPVLALFARVGFMLILVVPPLFVWKMGRLQYSCCVVULPDRLKXTNS-- 280
Db 427 ektpqntsklwl-----lvglciafaipfvlyaaaklfr--clnyvffr-slkpsssid 479
QY 281 -----PQR--LISCREEVDAC 295
Db 480 eyfseqplknlllstseeqlekc 502

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Search completed: October 12, 2001, 16:09:56  
Job time: 188 sec



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: October 12, 2001, 16:09:33 ; Search time 11.2 Seconds

(without alignments)  
951.201 Million cell updates/sec

Title: US-09-265-540E-2

Perfect score: 1627

Sequence: 1 MOTFTVLEIEITWTSLEFMWF.....VDACATVMSPEELLRAMIS 311

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	191	11.7	325	1	Q08334 homo sapien
2	178.5	11.0	337	1	ING5_HUMAN
3	178.5	11.0	590	1	INR1_MOUSE
4	170.5	10.5	349	1	1105_MOUSE
5	164.5	10.1	560	1	INR1_BOVIN
6	162.5	10.0	557	1	INR1_HUMAN
7	157.5	9.7	560	1	INR1_SHEEP
8	136	8.4	578	1	110R_HUMAN
9	130	8.0	292	1	TE_RABIT
10	125.5	7.7	295	1	TE_HUMAN
11	125.5	7.7	575	1	110R_MOUSE
12	121.5	7.5	289	1	TE_CAVPO
13	121	7.4	489	1	INGR_HUMAN
14	119.5	7.3	294	1	TE_MOUSE
15	114.5	7.0	292	1	TE_BOVIN
16	114	7.0	295	1	TE_RAT
17	114	7.0	507	1	EFOR_MOUSE
18	99	6.1	507	1	EFOR_RAT
19	97	6.0	508	1	EPOR_HUMAN
20	96	5.9	984	1	EPB1_HUMAN
21	96	5.9	984	1	EPB1_RAT
22	96	5.9	1447	1	DCX_MOUSE
23	95	5.8	1447	1	DCX_HUMAN
24	92.5	5.7	987	1	EPB4_HUMAN
25	89	5.5	831	1	PRLR_CHICK
26	89	5.5	977	1	EPB2_MOUSE
27	88.5	5.4	1928	1	LPH_RAT
28	88	5.4	902	1	EPBB_XENLA
29	88	5.4	985	1	EPAB_XENLA
30	87	5.3	984	1	EPB1_CHICK
31	86	5.3	227	1	COX2_HAPGR
32	86	5.3	227	1	COX2_LYCP1
33	86	5.3	227	1	COX2_RABIT

34	86	5.3	379	1	COS4_YEAST	P43542 saccharomyc
35	85.5	5.3	1630	1	PTPL_DROME	P35992 drosophila
36	85	5.2	227	1	COX2_CERS1	P03851 ceratotheri
37	85	5.2	227	1	COX2_DAMP	P06190 damaliscus
38	85	5.2	227	1	COX2_RHIN	O96190 rhinoceros
39	85	5.2	227	1	COX2_SHEEP	O78750 ovine
40	84.5	5.2	862	1	1125_HUMAN	O99665 homo sapien
41	84	5.2	227	1	COX2_GAPI	O37430 capra hircu
42	84	5.2	227	1	COX2_EQUAS	P92478 equus asinu
43	84	5.2	227	1	COX2_HORSE	P48660 equus cabal
44	84	5.2	227	1	COX2_MACRO	P92662 macropus ro
45	84	5.2	227	1	COX2_PROTA	P98042 propithecus

## ALIGNMENTS

RESULT	ID	Sequence	Standard	PRT	AA
1	1105_HUMAN	008334:			
AC	008334:	01-FEB-1995 (Rel. 31, Created)			
DT	01-FEB-1995 (Rel. 31, Last sequence update)				
DT	01-OCT-2000 (Rel. 40, Last annotation update)				
DE	INTERLEUKIN-10 RECEPTOR BETA CHAIN PRECURSOR (IL-10R-B) (IL-10R2)				
DE	(CYTOKINE RECEPTOR CLASS-II CRF2-4).				
GN	IL10RB OR CRF2-4.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Fetal brain;				
RX	MEDLINE=93300510; PubMed=8314576;				
RA	Lutalla G., Gardiner K., Uze G.;				
RT	"A new member of the cytokine receptor gene family maps on chromosome				
RT	21 at less than 35 kb from IFNAR.";				
RL	Genomics 16:366-373(1993).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=96054036; PubMed=7563119;				
RA	Lutalla G., McInnis M.G., Antonarakis S.E., Uze G.;				
RT	"Structure of the human CRF4 gene: comparison with its IFNAR				
RT	neighbor.";				
RL	J. Mol. Evol. 41:338-344(1995).				
RN	[3]				
RP	CHARACTERIZATION.				
RX	MEDLINE=97459974; PubMed=9312047;				
RA	Kotenko S.V., Krause C.D., Izotova L.S., Pollack B.P., Wu W.,				
RT	Pestka S.;				
RT	"Identification and functional characterization of a second chain of				
RT	the interleukin-10 receptor complex.";				
RL	EMBO J. 16:5894-5903(1997).				
CC	-1- FUNCTION: RECEPTOR FOR IL-10. SERVES AS AN ACCESSORY CHAIN				
CC	ESSENTIAL FOR THE ACTIVE IL-10 RECEPTOR COMPLEX AND TO INITIATE				
CC	IL-10-INDUCED SIGNAL TRANSDUCTION EVENTS.				
CC	-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.				
CC	-1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.				
CC	-1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.				
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CC	entities requires a license agreement (See http://www.isb-stb.ch/announce/				
CC	or send an email to license@isb-stb.ch).				
CC	EMBL; 217227; CAA78933.1; -				
DR	EMBL; 008988; AAA86872.1; -				
DR	PIR; A47003; A47003.				
DR	HSP; P13726; IDAN.				

DR MIM: 123889; -  
 KM Receptor; Transmembrane; Glycoprotein; Signal.  
 FT SIGNAL 1 19  
 FT CHAIN 20 325  
 FT DOMAIN 20 220  
 FT TRANSMEM 221 242  
 FT DOMAIN 243 325  
 FT DOMAIN 113 205  
 FT DISULFID 66 74  
 FT DISULFID 188 209  
 FT CARBOHYD 49 49  
 FT CARBOHYD 68 68  
 FT CARBOHYD 102 102  
 FT CARBOHYD 161 161  
 FT CONFLICT 124 124  
 FT CONFLICT 269 273  
 FT CONFLICT 274 325  
 SO SEQUENCE 325 AA; 37011 MW; 66706C79F8514B23 CRC64;  
 Query Match 11.7%; Score 191; DB 1; Length 325;  
 Best Local Similarity 26.6%; Pred. No. 8e-10;  
 Matches 77; Conservative 47; Mismatches 117; Indels 48; Gaps 16;  
 QY 12 WTSLFMWFYALLPCLLTDEVALIPAPONLSVSTNKKHLLMW-SPYIAGEYIYSEY 70  
 DB 3 W-SLGSW---LGGCLLSVALGAWPPENRNMSVNFKNILQWSPAFARQ-----NLTF 52  
 QY 71 QGEYESLYTSHIWPSSMCSLTGEGPCDVTDDITATVPYNLRATLGSQTSAN-SILKH 129  
 DB 53 TAOYLSTR-----IFQDKCNTLITLTCDFE-SLSKYGDHLIRVAERADEHSDWVNTFC 106  
 QY 130 PENRNSITLTPGMEIKKXGFHVLIEDLGPOFE-----FLVAYKRE 173  
 DB 107 PV--DDTIIGPGQVYVLADSL--HMRFLAPKLENEYETWTKMYNSMTYNQW--K 160  
 QY 174 PGAEHAKMVRSGGIPRLHETMERGAICYKAQTFVKAIGKYSASFQTECYE-VQGEAIP 232  
 DB 161 NGDEKFKQITPQYDFEY-LNRLEPWTYCVQVGRFLPDRNKAQMSBPVEQYTHDETFP 219  
 QY 233 ---LVLLAFVGVFMLILVVPVLF--VWKKGRLLQYSCCPVNVLPDILK 276  
 DB 220 SMWAVVILMASV-FWVCLALLGCESLIMCYKKTKVAFSPRNSLPQHLK 267  
 RESULT 2  
 INGS\_HUMAN STANDARD: PRT; 337 AA.  
 P38484;  
 01-OCT-1994 (Rel. 30, Created)  
 01-OCT-1994 (Rel. 30, Last sequence update)  
 01-OCT-2000 (Rel. 40, Last annotation update)  
 DE INTERFERON-GAMMA RECEPTOR BETA CHAIN PRECURSOR (INTERFERON-GAMMA  
 RECEPTOR ACCESSORY FACTOR-1) (AF-1) (INTERFERON-GAMMA TRANSDUCER-1).  
 GN IFNGR2 OR IFNGR1.  
 OS Homo sapiens (human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN 11  
 RP TISSUE FROM N.A.  
 RC TISSUE-Lung, fibroblast;  
 RX MEDLINE=94170380; PubMed=8124716;  
 RA Soh J., Donnelly R.J., Kotenko S., Mariano T.M., Cook J.R.,  
 Wang N., Emanuel S.L., Schwartz B., Miki T., Pestka S.;  
 RT Identification and sequence of an accessory factor required for  
 RT activation of the human interferon gamma receptor.;  
 RT Cell 76:793-802(1994).  
 RL 12  
 RN SEQUENCE OF 1-24 FROM N.A.  
 RP MEDLINE=97067142; PubMed=8910544;  
 RX Rhee S., Ebensperger C., Dembic Z., Pestka S.;  
 RT The structure of the gene for the second chain of the human

FT Interferon gamma receptor.;  
 RL J. Biol. Chem. 271:28947-28952(1996).  
 CC -1- FUNCTION: PART OF THE RECEPTOR FOR INTERFERON GAMMA. REQUIRED FOR  
 CC SIGNAL TRANSDUCTION. THIS ACCESSORY FACTOR IS AN INTEGRAL PART OF  
 CC THE IFN-GAMMA SIGNAL TRANSDUCTION PATHWAY AND IS LIKELY TO  
 CC INTERACT WITH GAF, JAK1, AND/OR JAK2.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.  
 CC -1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.  
 CC  
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 CC or send an email to [license@isb.slb.ch](mailto:license@isb.slb.ch)).  
 CC  
 CC EMBL; U05875; AAA16955.1; -;  
 CC EMBL; U05877; AAA16956.1; -;  
 DR EMBL; U68755; AAC52066.1; -;  
 DR MIM; 147569; -;  
 DR MIM; 209950; -;  
 DR InterPro: IPR001777; -;  
 DR Pfam; PF00041; fn3; 1.  
 DR Receptor; Transmembrane; Glycoprotein; Signal; Repeat.  
 FT SIGNAL 1 27  
 FT CHAIN 28 337  
 FT DOMAIN 28 247  
 FT TRANSMEM 248 268  
 FT TRANSMEM 269 337  
 FT DOMAIN 56 56  
 FT CARBOHYD 85 85  
 FT CARBOHYD 110 110  
 FT CARBOHYD 137 137  
 FT CARBOHYD 219 219  
 FT CARBOHYD 231 231  
 FT VARIANT 64 64  
 FT  
 FT  
 SO SEQUENCE 337 AA; 37834 MW; 18C61B10AD90E509 CRC64;  
 Query Match 11.0%; Score 178.5; DB 1; Length 337;  
 Best Local Similarity 26.1%; Pred. No. 1.1e-08;  
 Matches 75; Conservative 42; Mismatches 123; Indels 47; Gaps 14;  
 QY 11 IWTSLFMWFYALLPCLLTDEVALIPAPONLSVSTNKKHLLMSPYIAGEY--VYYSV 68  
 DB 6 LMSLLILGVRFAAAAAPPDPLSOLPAPQHKIRLYNMEVLSMEPVALSNTSPVYTRV 65  
 QY 69 EYGEYESLYTSHIWPSSMCSLTGEGPCDVTDDITATVP-----YNLRATLGS 119  
 DB 66 QFKYTSQWPLFADIMSIGVNCQTATATFC---DPTASPSAGFPMDNFVTLRLAEALGA 121  
 QY 120 QTSANSL---KHPPNRNSTLTPGMEIKKXGFHVL-----ELEDLGPOFE-FLVAY 169  
 DB 122 LHSAMVTPWPFQH--YRNVTVGPPENIEVTPGEGSLIIRFSSPFDIADTSTAFPCYYHY 179  
 QY 170 WXPREGAEHNR-NVRSGGIPVHLETMERGAICYKAQ-----TFKATIGYSAFSQT 221  
 DB 180 W--ERGGIQQYKGPFRNSI--SLDNLKPSRYVCQVQAOQLMKNKSNIFRGHLSNIS-- 233  
 QY 222 ECVEVGEA-IPVLYALPAFVGFMLILVVP---LFWKMGRLQY 263  
 DB 224 -CYETMDASRELQVILISVGTFSLSVLAGACFFYLKRYGLIKY 279  
 RESULT 3  
 INRL\_MOUSE STANDARD: PRT; 590 AA.  
 ID INRL\_MOUSE  
 AC P33896;  
 DT 01-FEB-1994 (Rel. 28, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)



DE 30-MAY-2000 (Rel. 39, Last annotation update)  
 DT INTERFERON-ALPHA/BETA RECEPTOR ALPHA CHAIN PRECURSOR (IFN-ALPHA-REC).  
 GN IFNARI OR IFNAR OR IFAR.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_Taxid:10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=92262522; PubMed=1539395;  
 RA Uze G., Lutfalla G., Bandu M.T., Proudhon D., Mogensen K.E.;  
 RT "Behavior of a cloned murine interferon alpha/beta receptor expressed  
 RT in homosppecific or heterosppecific background".  
 RL Proc. Natl. Acad. Sci. U.S.A. 89:4774-4778(1992).  
 CC -!- FUNCTION: RECEPTOR FOR INTERFERONS ALPHA AND BETA. BINDING TO TYPE  
 CC I IFNS TRIGGERS TYROSINE PHOSPHORYLATION OF A NUMBER OF PROTEINS  
 CC INCLUDING JAKs, TYK2, STAT PROTEINS AND IFN-R ALPHA-AND BETA-  
 CC SUBUNITS THEMSELVES.  
 CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -!- SIMILARITY: CONTAINS 2 FIBRONOCTIN TYPE III-LIKE DOMAINS.  
 CC -!- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.  
 CC -----  
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 CC or send an email to [license@isb-sdb.ch](mailto:license@isb-sdb.ch)).  
 CC -----  
 CC DR EMBL; M89641; AAA37890.1; -;  
 DR PIR; A45283; A45283.  
 DR MGD; MGI:107658; Ifnar.  
 KW Receptor; Transmembrane; Glycoprotein; Signal.  
 FT SIGNAL 1 26  
 FT CHAIN 27 590  
 FT  
 FT DOMAIN 27 429  
 FT TRANSMEM 430 449  
 FT DOMAIN 450 590  
 FT DISULFD 78 86  
 FT DISULFD 199 220  
 FT CARBOHYD 43 43  
 FT CARBOHYD 109 109  
 FT CARBOHYD 181 181  
 FT CARBOHYD 214 214  
 FT CARBOHYD 314 314  
 FT CARBOHYD 370 370  
 FT CARBOHYD 409 409  
 FT CARBOHYD 413 413  
 SEQUENCE 590 AA; 65776 MW; 7EC6DFF370185D3A CRC64;  
 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782

```

OY      237 LEAF-VGEFLLIVVPL-FVMKGRILQYSCCPVVLPDTLK---LTNSPOK---LISCR 289
       : | - :: || - | - | | | | | | | | | | | | | | | | | | | | | |
DB      433 ITGLGVFPFSNVAVIALRSVKM---YLCHVCPPPLPKPRSIDFFSEPPSKNVLITAE 489
OY      290 -----EVDACATAVN-SPEELLRAWIS 311
Db      490 HTERCFIENFTDVAVEVKAHEEDLRKYS 520

RESULT   4
ID        I10S_MOUSE          STANDARD:          PRT:         349 AA.
AC        Q61190;
DT        01-OCT-2000 (Rel. 40, Created)
DT        01-OCT-2000 (Rel. 40, Last sequence update)
DT        01-OCT-2000 (Rel. 40, Last annotation update)
DE        INTERLEUKIN-10 RECEPTOR BETA CHAIN PRECURSOR (IL-10R-B) (II-10R2)
GN        IL10RB OR CREB4.
OS        Mus musculus (Mouse).
OC        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC        Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX        NCBI_TaxID=10090;
RN        [1]
RP        SEQUENCE FROM N.A.
RX        MEDLINE=97199375; PubMed=9047351;
RA        Gibbs V.C., Pennica D.;
RT        "CRP2-4: Isolation of cDNA clones encoding the human and mouse
RL        proteins."
RM        Gene 186:97-101(1997).
RN        [2]
RP        CHARACTERIZATION.
RX        MEDLINE=98130620; PubMed=9463407;
RA        Spencer S.D., Di Marco F., Hooley J., Pitts-Meek S., Bauer M.,
RA        Ryan A.M., Sordat B., Gibbs V.C., Agnet M.;
RT        "The orphan receptor CRP2-4 is an essential subunit of the interleukin
RT        10 receptor."
RL        J. Exp. Med. 187:571-578(1998).
CC        -1- FUNCTIONAL: RECEPTOR FOR IL-10. SERVES AS AN ACCESSORY CHAIN
CC        ESSENTIAL FOR THE ACTIVE IL-10 RECEPTOR COMPLEX AND TO INITIATE
CC        IL-10-INDUCED SIGNAL TRANSDUCTION EVENTS.
CC        -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC        -1- SIMILARITY: CONTAINS 2 FIROREACTIN TYPE III-LIKE DOMAINS.
CC        -1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
CC        CC
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CC        or send an email to license@sib-sib.ch).
CC        CC
DR        EMBL; U53696; AAC53062.1; -.
DR        MGD; MG1:109380; IL10rb.
DR        InterPro; IPRO000282; -.
DR        InterPro; IPRO01777; -.
DR        Pfam; PF00041; fn3; 1.
KW        Receptor; Transmembrane; Glycoprotein; Signal.
FT        SIGNAL                     1..19             POTENTIAL.
FT        CHAIN                      20..349           EXTRACELLULAR.
FT        DOMAIN                     20..220           INTERLEUKIN-10 RECEPTOR BETA CHAIN.
FT        TRANSMEM                    221..241         CYTOPLASMIC (POTENTIAL).
FT        DOMAIN                     242..349         FIBONECTIN TYPE-III.
FT        DOMAIN                     113..205         BY SIMILARITY.
FT        DISULFID                     66..74           BY SIMILARITY.
FT        CARBOHYD                     49              N-LINKED (GLCNAC. . . ) (POTENTIAL).
FT        CARBOHYD                     102             N-LINKED (GLCNAC. . . ) (POTENTIAL).
FT        CARBOHYD                     161             N-LINKED (GLCNAC. . . ) (POTENTIAL).
FT        CARBOHYD                     199             N-LINKED (GLCNAC. . . ) (POTENTIAL).
SQ        SEQUENCE                   349 AA; 39774 MW; 5BBAAFB8B6330A39 CRC64;
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RL Cell 60:225-234(1990).  
 RA [2]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=92129376; PubMed=1370833;  
 RA Lutfalla G., Gardiner K., Proudhon D., Vielh E., Uze G.;  
 RT "The structure of the human interferon alpha/beta receptor gene.";  
 RL J. Biol. Chem. 267:2802-2809(1992).  
 RM [3]  
 RP PHOSPHORYLATION BY TYK2.  
 RA MEDLINE=95059042; PubMed=7526154;  
 RA Colomonic O., Yan H., Domanski P., Handa R., Smalley D.,  
 RA Mullerman J., Witte M., Krishnan K., Krolewski J.;  
 RT "Direct binding to and tyrosine phosphorylation of the alpha subunit  
 of the type I interferon receptor by p135tyk2 tyrosine kinase.";  
 RL Mol. Cell. Biol. 14:8133-8142(1994).  
 CC -I- FUNCTION: RECEPTOR FOR INTERFERONS ALPHA AND BETA. BINDING TO TYPE  
 CC I FENS TRIGGERS TYROSINE PHOSPHORYLATION OF A NUMBER OF PROTEINS  
 CC INCLUDING JAKS, TYK2, STAT PROTEINS AND IFN-R ALPHA-AND BETA-  
 CC SUBUNITS THEMSELVES.  
 CC -I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -I- TISSUE SPECIFICITY: IFN RECEPTORS ARE PRESENT IN ALL TISSUES AND  
 CC EVEN ON THE SURFACE OF MOST IFN-RESISTANT CELLS.  
 CC -I- PTM: PHOSPHORYLATED ON TYROSINE RESIDUES BY TYK2 TYROSINE KINASE.  
 CC -I- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.  
 CC -I- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.  
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 CC -----  
 DR EMBL: J03171; AAA52730.1; -  
 DR EMBL: X60459; CAA42992.1; -  
 DR PIR: A32694; A32694.  
 DR PIR: S17112; S17112.  
 DR MIM: 107450; -  
 KM Receptor; Transmembrane; Glycoprotein; Signal; Polymorphism;  
 KM Phosphorylation.  
 FT SIGNAL 1 27  
 FT CHAIN 28 557  
 FT DOMAIN 28 436  
 FT TRANSMEM 437 457  
 FT DOMAIN 458 557  
 FT DISULFID 79 87  
 FT DISULFID 199 220  
 FT MOD\_RES 466 466  
 FT MOD\_RES 481 481  
 FT CARBOHYD 50 50  
 FT CARBOHYD 58 58  
 FT CARBOHYD 81 81  
 FT CARBOHYD 88 88  
 FT CARBOHYD 110 110  
 FT CARBOHYD 172 172  
 FT CARBOHYD 254 254  
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 FT CARBOHYD 314 314  
 FT CARBOHYD 376 376  
 FT CARBOHYD 416 416  
 FT CARBOHYD 433 433  
 FT VARIANT 168 168  
 FT L -> V.  
 FT /FTID=VAR\_002717.  
 FT CONFLICT 17 17 G -> A (IN REF. 2)  
 FT SEQUENCE 557 AA: 63525 MM: 056744C8A1ADEB73 CRC64;

Query Match 10.0%; Score 162.5; DB 1; Length 557;  
 Best Local Similarity 22.0%; Pred. No. 5.2e-07;  
 Matches 71; Conservative 54; Mismatches 115; Indels 83; Gaps 17;

QY 21 YALPCLLTDEVALIPAPQNLSTVSTNKKHLMSPTVAPBETVYYSVEQGEYSLYT- 79  
 Db 215 YSPVHCIKTYENELPPENIEVSQNONVYWK- DITYANMTFQVOMHAFLK 267  
 QY 80 -SHIWIPESWCSLFGPCDVTDDITATVPYN-----LRVATLSQTSAMS- 125  
 Db 268 RNPQNHLT--KMQOI--PCCENKTTQCYFPQVPOVFOKGILYLLKQVSDGNTSFMSEE 321  
 QY 126 -----ILKHPFNSTILTRPGMEIKXKGFHLY-----ELEDLGPQEF 165  
 Db 322 IKPDTIQAFLLPPVFNRS-----LSDSFHITIGAPKQSGNPVIQDYLYIE- 370  
 QY 166 LVATWXPGEAEHVKWVRSGCIPVHLETMGAAVCYKAO--TFVKAIGXSAFSQTEC 223  
 Db 371 -IIFWENTSNAERKIIETK--DVTVPNLKPLVYCYKARAHMDEKLNSSVFSDAVC 426  
 QY 224 VEVO-GEAIPVYLAFVGFMLILVYVPLVWKMGRLLQSCPPVYLPPTLKTSN- 280  
 Db 427 EKTRPGNTSKTWL-----IVGICIALFALPFIYIAKAYFLR--CLNYVEFP-SLKPSISID 479  
 QY 281 -----PQK--LISCRREVDAC 295  
 Db 480 EYFSEQPLKNLLSTSEQIEKC 502  
 RESULT 7  
 INRL SHEEP STANDARD; PRT; 560 AA.  
 ID 028589: 095206;  
 AC 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE INTERFERON-ALPHA/BETA RECEPTOR ALPHA CHAIN PRECURSOR (IFN-ALPHA-REC)  
 DE (INTERFERON-ALPHA/BETA RECEPTOR-1).  
 GN IFNARI OR IFNAR.  
 OS Ovis aries (Sheep).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Caprinae; Ovis.  
 OX NCBI\_Taxid=9940;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-Endometrium;  
 RX MEDLINE=97135690; PubMed=8981227;  
 RA Kaluz S., Fisher P.A., Kaluzova M., Sheldrick E.L., Flint A.P.F.;  
 RT "Structure of an ovine interferon receptor and its expression in  
 RT endometrium.";  
 RL J. Mol. Endocrinol. 17:207-215(1996).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-Endometrium;  
 RX MEDLINE=98006426; PubMed=9348203;  
 RA Han C.-S., Mathialagan N., Klemann S.W., Roberts R.M.;  
 RT "Molecular cloning of ovine and bovine type I interferon receptor  
 RT subunits from uteri, and endometrial expression of messenger  
 RT ribonucleic acid for ovine receptors during the estrous cycle and  
 RT pregnancy.";  
 RL Endocrinology 138:4757-4767(1997).  
 CC -I- FUNCTION: RECEPTOR FOR INTERFERONS ALPHA AND BETA. BINDING TO TYPE  
 CC I FENS TRIGGERS TYROSINE PHOSPHORYLATION OF A NUMBER OF PROTEINS  
 CC INCLUDING JAKS, TYK2, STAT PROTEINS AND IFN-R ALPHA-AND BETA-  
 CC SUBUNITS THEMSELVES.  
 CC -I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -I- TISSUE SPECIFICITY: EXPRESSED IN ALL TISSUES EXAMINED EXCEPT  
 CC CONCEPTUS AT DAY 15 OF PREGNANCY.  
 CC -I- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.  
 CC -----  
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DT 01-MAR-1992 (Rel. 21, Created)  
 DT 01-MAR-1992 (Rel. 21, Last sequence update)  
 DT 01-OCT-2000 (Rel. 40, Last annotation update)  
 DE TISSUE FACTOR PRECURSOR (TF) (COAGULATION FACTOR III).  
 GN F3.  
 OS Oryctolagus cuniculus (Rabbit).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 OX NCBI\_TaxID=9986;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-Heart;  
 RX MEDLINE=91200676; PubMed=1840552;  
 RA Andrews B.S., Kenemulla A., Fowler B.J., Edgington T.S., Mackman N.;  
 RT "Conservation of tissue factor primary sequence among three mammalian  
 species.";  
 RL Gene 98:265-269(1991).  
 RN [2]  
 RP SEQUENCE OF 33-292 FROM N.A.  
 RC STRAIN=NEW ZEALAND WHITE; TISSUE=Brain;  
 RX MEDLINE=92081032; PubMed=1746002;  
 RA Pavashe A., Ezekowitz M., Lin T.C., Horton R., Bach R., Konigsberg W.;  
 RT "Molecular cloning, characterization and expression of cDNA for  
 rabbit brain tissue factor.";  
 RL Thromb. Haemost. 66:315-320(1991).  
 RN [3]  
 RP X-RAY CRYSTALLOGRAPHY (2.35 ANGSTROMS) OF 36-240.  
 RX MEDLINE=98266351; PubMed=9605315;  
 RA Muller Y.A., Kelley R.F., de Vos A.M.;  
 RT "Hinge bending within the cytokine receptor superfamily revealed by  
 the 2.4 A crystal structure of the extracellular domain of rabbit  
 tissue factor.";  
 RL Protein Sci. 7:1106-1115(1998).  
 CC -1- FUNCTION: INITIATES BLOOD COAGULATION BY FORMING A COMPLEX WITH  
 CIRCULATING FACTOR VII OR VIIA. THE [TF-VIIA] COMPLEX ACTIVATES  
 FACTORS IX OR X BY SPECIFIC LIMITED PROTEOLYSIS. TF PLAYS A ROLE IN  
 NORMAL HEMOSTASIS BY INITIATING THE CELL-SURFACE ASSEMBLY AND  
 PROPAAGATION OF THE COAGULATION PROTEASE CASCADE.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- TISSUE SPECIFICITY: BRAIN, HEART.  
 CC -1- SIMILARITY: BELONGS TO THE TISSUE FACTOR FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL; M55390; AAA63469.1; .  
 DR EMBL; X53521; .; NOT\_ANNOTATED\_CDS.  
 DR PIR; J00441; KFRB3.  
 DR PIR; S23681; S23681.  
 DR PDB; 1A21; 27-MAY-98.  
 DR InterPro; IPR001187; .  
 DR Pfam; PF01108; Tissue\_fac; 1.  
 DR PRINTS; PRO0346; TISSUEFACTOR.  
 DR PROSITE; PS00621; TISSUE\_FACTOR; 1.  
 KW Glycoprotein; Blood coagulation; Transmembrane; Signal; Lipoprotein;  
 KW Palmitate; 3D-structure.  
 FT CHAIN 1 32  
 FT SIGNAL 1 32  
 FT CHAIN 33 292  
 FT DOMAIN 33 250  
 FT TRANSMEM 251 271  
 FT DOMAIN 272 292  
 FT SITE 44 46  
 FT SITE 75 77  
 FT CARBOHYD 41 41  
 FT CARBOHYD 114 114  
 FT CARBOHYD 154 154  
 FT CARBOHYD 167 167  
 FT CARBOHYD 182 182  
 TISSUE FACTOR.  
 EXTRACELLULAR (POTENTIAL).  
 POTENTIAL.  
 CYTOPLASMIC (POTENTIAL).  
 WKS MOTIF.  
 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT DISULFID 79 87  
 FT LIPID 216 239  
 FT LIPID 274 274  
 SQ SEQUENCE 292 AA; 32738 MW; 4860A1CDBACFF71 CRC64;  
 Query Match 8.08; Score 130; DB 1; Length 292;  
 Best Local Similarity 24.0%; Pred. No. 0.00019;  
 Matches 61; Conservative 34; Mismatches 101; Indels 58; Gaps 11;  
 QY 40 NLVLSTNNMHLMMSPVIAAGETVYVSVYQGESELYSHI-----WIPSSMCSTLE 93  
 DB 41 NLVLSTNNMHLMMSPVIAAGETVYVSVYQGESELYSHI-----WIPSSMCSTLE 83  
 QY 94 GPCDWDYDDTATVY--PYNLVRATLGSQTSAMSILKHPFRNS-----TILTRPGM 143  
 DB 84 ETECDLDEYVKDVGQYMARVLSYPARNGTTCFPPEPRRNSPEFTPYDNLGQPTI 143  
 QY 144 E-IXKGFHLVLEED-----IGPQFEPLVAYXREPGAEHVKVRS 185  
 DB 144 QSEQVQTKLNTVQDARTLVRRNGTFLSLRAVKGDLNTLYYWR-----ASTGKKVAT 199  
 QY 186 GGIPIVHEHPEPAAYGVKQTFV--KAIGKYSFSTECV--EVQGAIPLYALPAFVG 242  
 DB 200 TTNTEFLIDYDKGENYCFVQAVIPSRKRQSPESLTECTSRQGRAREMFTIGAVV 259  
 QY 243 FMLIVVPLFVWK 256  
 DB 260 VALLIIVSTVYK 273  
 RESULT 10  
 TF\_HUMAN  
 ID TF\_HUMAN STANDARD; PRT; 295 AA.  
 AC P13726;  
 DT 01-JAN-1990 (Rel. 13, Created)  
 DT 01-JAN-1990 (Rel. 13, Last sequence update)  
 DT 01-OCT-2000 (Rel. 40, Last annotation update)  
 DE TISSUE FACTOR PRECURSOR (TF) (COAGULATION FACTOR III)  
 DE (THROMBOPLASTIN) (CD142 ANTIGEN).  
 GN F3.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=89247359; PubMed=2719931;  
 RA Mackman N., Morrissey J.H., Fowler B., Edgington T.S.;  
 RT "Complete sequence of the human tissue factor gene, a highly  
 RT regulated cellular receptor that initiates the coagulation protease  
 RT cascade.";  
 RL Biochemistry 28:1755-1762(1989).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=87260946; PubMed=3037536;  
 RA Spicer E.K., Horton R., Bloem L., Bach R., Williams K.R., Guha A.,  
 RA Kraus J., Lin T.C., Nemerson Y., Konigsberg W.H.;  
 RT "Isolation of cDNA clones coding for human tissue factor: primary  
 RT structure of the protein and cDNA.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 84:5148-5152(1987).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=87244317; PubMed=3297348;  
 RA Morrissey J.H., Fakhrat H., Edgington T.S.;  
 RT "Molecular cloning of the cDNA for tissue factor, the cellular  
 RT receptor for the initiation of the coagulation protease cascade.";  
 RL Cell 50:129-135(1987).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=88050796; PubMed=2823875;  
 RA Scarpati E.M., Wen D., Broze G.J. Jr., Miletich J.P.,  
 RA Flandermeier R.R., Siegel N.R., Sadler J.E.;

RT Human tissue factor: cDNA sequence and chromosome localization of  
 the gene." ;  
 RL Biochemistry 26:5234-5238(1987).  
 [5]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=88100453; PubMed=3424286;  
 RA Fisher K.L., Gorman C.M., Venar G.A., O'Brien D.P., Lavan R.M.;  
 RT "Cloning and expression of human tissue factor cDNA." ;  
 RL Thromb. Res. 48:89-99(1987).  
 [6]  
 RP DISULFIDE BONDS, AND PALMITOYLATION.  
 RX MEDLINE=89000604; PubMed=3166978;  
 RA Bach R., Konigsberg W.H., Nemerson Y.;  
 RT "Human tissue factor contains thioester-linked palmitate and stearate  
 on the cytoplasmic half-cysteine." ;  
 RL Biochemistry 27:4227-4231(1988).  
 [7]  
 RP X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS) OF 33-243.  
 RX MEDLINE=94368785; PubMed=8086403;  
 RA Muller Y.A., Ullsch M.H., Kelley R.F., de Vos A.M.;  
 RT "Structure of the extracellular domain of human tissue factor:  
 location of the factor VIIa binding site." ;  
 RL Biochemistry 33:10864-10870(1994).  
 [8]  
 RP X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS) OF 33-243.  
 RX MEDLINE=96190957; PubMed=8609606;  
 RA Muller Y.A., Ullsch M.H., de Vos A.M.;  
 RT "The crystal structure of the extracellular domain of human tissue  
 factor refined to 1.7-A resolution." ;  
 RL J. Mol. Biol. 256:144-159(1996).  
 [9]  
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 33-251 IN COMPLEX WITH FVIIA.  
 RX MEDLINE=96175641; PubMed=8598903;  
 RA Banner D.W., D'Arcy A., Chene C., Winkler F.K., Guha A.;  
 RA Konigsberg W.H., Nemerson Y., Kirchhofer D.;  
 RT "The crystal structure of the complex of blood coagulation factor  
 VIIa with soluble tissue factor." ;  
 RL Nature 380:41-46(1996).  
 [10]  
 RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 37-242 IN COMPLEX WITH FVIIA.  
 RX MEDLINE=99126538; PubMed=9925787;  
 RA Zhang E., St Charles R., Tulinsky A.;  
 RT "Structure of extracellular tissue factor complexed with factor VIIa  
 inhibited with a BPTI mutant." ;  
 RL J. Mol. Biol. 285:2089-2104(1999).  
 [11]  
 RP -1- FUNCTION: INITIATES BLOOD COAGULATION BY FORMING A COMPLEX WITH  
 CIRCULATING FACTOR VII OR VIIA. THE (TF-VIIA) COMPLEX ACTIVATES  
 FACTORS IX OR X BY SPECIFIC LIMITED PROTEOLYSIS. TF PLAYS A ROLE IN  
 NORMAL HEMOSTASIS BY INITIATING THE CELL-SURFACE ASSEMBLY AND  
 PROPAGATION OF THE COAGULATION PROTEASE CASCADE.  
 CC SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- INDICATION: TF EXPRESSION IS HIGHLY DEPENDENT UPON CELL TYPE. TF  
 CAN ALSO BE INDUCED BY THE INFLAMMATORY MEDIATORS INTERLEUKIN 1  
 AND TNF. AS WELL AS BY ENDOTOXIN, TO APPEAR ON MONOCYTES AND  
 VASCULAR ENDOTHELIAL CELLS AS A COMPONENT OF CELLULAR IMMUNE  
 RESPONSE.  
 CC -1- SIMILARITY: BELONGS TO THE TISSUE FACTOR FAMILY.  
 CC -1- DATABASE: NAME-PROT; NOTE-CD guide CD142 entry;  
 WWW="http://www.ncbi.nlm.nih.gov/protow/CD/CD142.htm".  
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 or send an email to license@isb-sib.ch).  
 CC EMBL: J02931; AAA61150.1; -  
 DR EMBL: M16553; AAA61151.1; -  
 DR EMBL: J02846; AAA61152.1; -  
 DR EMBL: M27436; AAA36734.1; -  
 DR EMBL: A19048; CAA01438.1; -

DR PIR: A28320; KFH03.  
 DR PIR: A43645; A43645.  
 DR PIR: A47574; A47574.  
 DR PDB: 1BOY; 10-JUN-96.  
 DR PDB: 2HFT; 29-JAN-96.  
 DR PDB: 1DAN; 04-SEP-97.  
 DR PDB: 1AHW; 19-AUG-98.  
 DR PDB: 1TFH; 19-AUG-98.  
 DR PDB: 1FAK; 03-DEC-99.  
 DR PMID: 134390.  
 DR InterPro: IPR001187.  
 DR Pfam: PF01108; Tissue\_fac. 1.  
 DR PRINTS: PR00346; TISSUEFACTOR.  
 DR PROSITE: PS00621; TISSUE\_FACTOR. 1.  
 KW Glycoprotein; Blood coagulation; Transmembrane; Signal; Lipoprotein;  
 RL Palmitate; 3D-structure.  
 FT SIGNAL 1 32  
 FT CHAIN 33 295  
 FT DOMAIN 33 251  
 FT TRANSMEM 252 274  
 FT DOMAIN 275 295  
 FT SITE 46 48  
 FT SITE 77 79  
 FT SITE 190 192  
 FT CARBOHYD 156 156  
 FT CARBOHYD 169 169  
 FT DISULFID 81 89  
 FT DISULFID 218 241  
 FT LIPID 277 277  
 FT CONFLICT 260 260  
 FT SEQUENCE 295 AA; 33067 MW; D3486C713ED8AD0 CRC64;  
 QUERY MATCH 7.7%; Score 125.5; DB 1; Length 295;  
 Best Local Similarity 23.4%; Pred. No. 0.00049;  
 Matches 63; Conservative 35; Mismatches 122; Indels 49; Gaps 12;

QY 13 TSLFMFVYALIPCLLTDEVALTPAPONLSVLTNNKHLMSPVYIAPGEVYSYVYOG 72  
 DB 19 TLLGWFVAQVAGAGSTNTV--AAVNLTKWSTNKTLEMEP--KPVNOY-YTVQIST 72  
 QY 73 EYESLYTHIMIPSSWCSLTSPCEDVDDITATV--PNNLVKATLGSQTSNLSLKRP 130  
 DB 73 K-----SGDW--KSKCFYTDTECDLDEIVKQVYIARVFSYPAGNVSTGSAGRP 124  
 QY 131 FNRRS-----TLTRPGME-IKKXGPHVIELED-----LGPPE 164  
 DB 125 LYENSPEFTPYLETNLGPTIOSFEQVGTKNVYVEDERTLYRRNTFLSLDVFCKDL 184  
 QY 165 FLVAYMXREPGAEEHVKNVRSGLIPVHETMEGAAYCVKAQTFV--KAIGYSAFSQTE 222  
 DB 185 YLYLVWKKSSSSSKTKAKT-----NTNEFLDVGKNGYCVQAVISRVNKRSTDSPE 240  
 QY 223 CV-EVQGEAIPVYVLAFLAFVGMILIVV 250  
 DB 241 CMGQKGEFERELFYIIGAVVFVILVIL 269  
 RESULT 11  
 ID 11OR\_MOUSE STANDARD: PRT; 575 AA.  
 AC 061727;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 01-OCT-2000 (Rel. 40, Last annotation update)  
 DE INTERLEUKIN-10 RECEPTOR ALPHA CHAIN PRECURSOR (IL-10R-A) (IL-10R1).  
 GN IL10RA OR IL10R.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.

CC	STRAIN=C57BL/6 X AJ F1; TISSUE=Hematopoietic;	
RX	MEDLINE=94068585; Pubmed=8248239;	
RA	Ho A.S.-Y., Liu Y., Khan T.A., Hsu D.-H., Bazan J.F., Moore K.W.;	
RT	"A receptor for Interleukin 10 is related to interferon receptors."	
RL	Proc. Natl. Acad. Sci. U.S.A. 90:11267-11271(1993).	
CC	-1- FUNCTION: RECEPTOR FOR IL-10; BINDS IL-10 WITH A HIGH AFFINITY.	
CC	-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.	
CC	-1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.	
CC	-----	
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CC	or send an email to <a href="mailto:license@isb.ch">license@isb.ch</a> ).	
CC	-----	
DR	EMBL; L12120; AAA16156.1; -	
DR	MGD; MGI:96538; 1110ra.	
KW	Receptor; Transmembrane; Glycoprotein; Signal.	
FT	CHAIN 1 16 POTENTIAL.	
FT	SIGNAL 17 575	
FT	DOMAIN 17 241 INTERLEUKIN-10 RECEPTOR ALPHA CHAIN.	
FT	TRANSMEM 242 262 EXTRACELLULAR (POTENTIAL).	
FT	DOMAIN 263 575 CYTOPLASMIC (POTENTIAL).	
FT	DISULFID 204 225 POTENTIAL.	
FT	CARBOHYD 50 50 N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	CARBOHYD 66 66 N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	CARBOHYD 113 113 N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	CARBOHYD 182 182 N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	CARBOHYD 238 238 N-LINKED (GLCNAC. . .) (POTENTIAL).	
CC	SEQUENCE 575 AA; 64248 MW; 820B9CDD576F686B7 CRC64;	

Query Match	7.7%: Score 125.5; DB 1; Length 575;
Best Local Similarity	20.4%: Pred. No. 0.0011:
Matches	64; Conservative 53; Mismatches 121; Indels 75; Gaps 12.
QY	23 LIPCLLT-----DEVAI--LPAPONLSVLSNNKHHLMMSPIAPGRTVYVSVEYOGF 73
Db	1 LIPFVLTISSLERLAVGTETLPSVYVFEARFQHLLHMKPIPNQSESTVEYVALK-- 62
QY	74 YESLYTSIMWIPSSWCSLTEGECVY----DDITATVYPYNLRVATLGSOTSAMSILKH 129
Db	63 --QYGNSTWMDIHICRKAQALSCDLTFTTDLVHRSYGYRARAIVADVNSQYSNNMTTET 119
QY	130 PENRSTLT-----RPGMEIKKKGFHLVTELEDGDPQEFVLVAWY 171
Db	120 RFTYDEVILTFVDSVTLKMGDIYGTTHPRPTTPADDEREYQVFKDL-RVYKISIRKFS 178
QY	172 REPAAEEHVKM-VRSGGIPVHLETMEPGAAYCAVKQOTVKAIGXYSASFQTECEVGEA 230
Db	179 ELKNATRKVKQETFLVYPIGVR-----KKCVKLLPRLESINKNAEHSBECCLITTEQ 232
QY	231 I-----PLVALFAFYVGMILVWVBLFYVWKMGRLLOYSCCPVYV----- 271
Db	233 YETVNTLSILVISMFLFCG-ILVCLVLYQWYIRHPGKL-----PLVLFVKRPHDFPAMP 285
QY	272 -----PDTLKITN 279
Db	286 LCPETPDALHIVD 298
RESULT 12	
TF_CAVPO	STANDARD; PRT; 289 AA.
AC	Q9JUL08;
DT	01-OCT-2000 (Rel. 4.0, Created)
DT	01-OCT-2000 (Rel. 4.0, Last sequence update)
DT	01-OCT-2000 (Rel. 4.0, Last annotation update)
DE	TISSUE FACTOR PRECURSOR (TF) (COAGULATION FACTOR III).
GN	F3.
OS	Cavia porcellus (Guinea pig).

CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC	Mammalia; Eutheria; Rodentia; Hystriocognathi; Cavidae; Cavia.
OX	NCBI_TaxID=10141;
RN	(1)
RP	SEQUENCE FROM N.A.
RC	TISSUE=Lung;
RX	MEDLINE=20206020; PubMed=10744153;
RA	Shi R.J., Li W.Z., Marder V.J., Sporn L.A.;
RT	"Cloning of guinea pig tissue factor cDNA: comparison of primary
RT	structure among six mammalian species.";
RL	Thromb. Haemost. 83:455-461(2000).
CC	-1- FUNCTION: INITIATES BLOOD COAGULATION BY FORMING A COMPLEX WITH
CC	CIRCULATING FACTOR VII OR VIII. THE [TF:VIIA] COMPLEX ACTIVATES
CC	FACTORS IX OR X BY SPECIFIC LIMITED PROTOCOLS. TF PLAYS A ROLE IN
CC	NORMAL HEMOSTASIS BY INITIATING THE CELL-SURFACE ASSEMBLY AND
CC	PROPAagation OF THE COAGULATION PROTEASE CASCADE.
CC	-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC	-1- SIMILARITY: BELONGS TO THE TISSUE FACTOR FAMILY.
-----	
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CC	or send an email to <a href="mailto:license@isb.sib.ch">license@isb.sib.ch</a> ).
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CC	EMBL; AF131949; AAF36523.1; "-
DR	InterPro; IPRO01187; "-
DR	Pfam; PF01108; TISSUE_FAC1.
DR	PRINTS; PRO0346; TISSUEFACTOR
DR	PROSITE; PS00621; TISSUE_FACTOR; FALSE_NEG.
KW	Glycoprotein; Blood coagulation; Transmembrane; Signal; Lipoprotein;
KW	Palmitate.
FT	SIGNAL
FT	CHAIN
FT	DOMAIN
FT	TRANSNM
FT	DOMAIN
FT	SIZE
FT	STATE
FT	CARBOHYD
FT	CARBOHYD
FT	CARBOHYD
FT	CARBOHYD
FT	DISULFID
FT	LIPID
FO	SEQUENCE
FT	1
FT	32
FT	33
FT	247
FT	268
FT	269
FT	289
FT	44
FT	46
FT	75
FT	77
FT	41
FT	41
FT	111
FT	151
FT	164
FT	79
FT	87
FT	213
FT	236
FT	271
FO	289 AA; 32456 MW; TAB97/F8E5B195FE1 CRC64;
FT	BY SIMILARITY.
FT	TISSUE FACTOR.
FT	EXTRACELLULAR (POTENTIAL).
FT	POTENTIAL.
FT	CYTOPLASMIC (POTENTIAL).
FT	WKS MOTIF.
FT	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	BY SIMILARITY.
FT	BY SIMILARITY.
FT	PALMITATE (BY SIMILARITY).

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Query Match          7.5%; Score 121.5; DB 1; Length 289;
Match Local Similarity 24.4%; Pred. No. 0.0011;
Matches 69; Conservative 35; Mismatches 98; Indels 81; Gaps 16;

QY 22 ALIPOLLDEVAALPA-----PONSVLSTNNKHLHMSPYIAPGEIYVSVEYOG 73
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 15 AVPEPTLLIGWLVQYAGAGIIPVKRYNTLTKWSTNKTILEMEP--KPINNV-YTVQ 71
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY 74 YESLYTSHIMIPSSKCSLTGECBDYDDITATV--PYNLVRYATLGSQTSAMSLIKPF 131
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 72 LED-?-?-?-W-KSICFEITATECCLISEMAMPNVOQTFLARVISILPNSST--G 120
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY 132 NRNS-----TILTRGMEIYK-XGPHLIELED-----LGPQDEF 165
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 121 YSNSPEPTPYOETNLGQPKISFKLVGKTLNVYADTOLTARSGTFLSLDITFGKNLQY 180
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY 166 LVAYXRPGEAENHKAVRSGCIVPHLETMEPGAACYCAKTFYKAI-----GXYSAFS 219
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 181 MLYYV-RSSTGTGKTAMNTNEF---LLDVQGDQD-----FYQAVIPSRKDKKKSSES 232
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY 220 QTECV-----EVQGEAIPLVLALEAFVGFMLLVVYVPLVF 254
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

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DB 233 ITVCTLEKGRKREMSRIVVPVL-----VTVVIALFL 266

RESULT 13  
INGR. HUMAN STANDARD; PRT; 489 AA.  
AC P15260;  
DT 01-APR-1990 (Rel. 14, Created)  
DT 01-APR-1990 (Rel. 14, Last sequence update)  
DT 01-OCT-2000 (Rel. 40, Last annotation update)  
DE INTERFERON-GAMMA RECEPTOR ALPHA CHAIN PRECURSOR (CDW119).  
GN IFNGR1.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP MEDLINE=89003065; PubMed=2971451;  
RT Aguet M., Dembic Z., Merlin G.;  
RL "Molecular cloning and expression of the human interferon-gamma  
receptor.";  
RN [2]  
RP DISULFIDE BONDS, PARTIAL SEQUENCE, AND MUTAGENESIS.  
RN MEDLINE=93183911; PubMed=8443182;  
RT Stueber D., Friedlein A., Fountoulakis M., Lahm H.-W., Garotta G.;  
RT "Alignment of disulfide bonds of the extracellular domain of the  
interferon gamma receptor and investigation of their role in  
biological activity.";  
RL Biochemistry 32:2423-2430(1993).  
RN [3]  
RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 26-248.  
RN MEDLINE=95342235; PubMed=7617032;  
RT Walter M.R., Windsor W.T., Nagabushan T.L., Lundell D.J., Lunn C.A.,  
RA Zaudony P.J., Narula S.K.;  
RL "Crystal structure of a complex between interferon-gamma and its  
soluble high-affinity receptor.";  
RN Nature 376:230-235(1995).  
RN [4]  
RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 28-122 COMPLEX WITH ANTIBODY.  
RN MEDLINE=98035727; PubMed=9367779;  
RT Sogabe S., Stuart F., Henke C., Bridges A., Williams G., Birch A.,  
RA Winkler F.K., Robinson J.A.;  
RT "Neutralizing epitopes on the extracellular interferon gamma receptor  
(IFNgammaR) alpha-chain characterized by homolog scanning mutagenesis  
and x-ray crystal structure of the A6 fab-IFNgammaR1-108 complex.";  
RN J. Mol. Biol. 273:882-897(1997).  
RN [5]  
RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF COMPLEX WITH ING.  
RN PubMed=10986460;  
RT Thiel D.J., Le Du M.-H., Walter R.L., D'Arcy A., Chene C.,  
RA Fountoulakis M., Garotta G., Winkler F.K., Falick S.E.;  
RT "Observation of an unexpected third receptor molecule in the crystal  
structure of human interferon-gamma receptor complex.";  
RL Structure 8:927-936(2000).  
RN [6]  
RP FUNCTION: RECEPTOR FOR INTERFERON GAMMA. TWO RECEPTORS BIND ONE  
INTERFERON-GAMMA DIMER.  
CC [1]  
CC SUBUNIT: MONOMER.  
CC [2]  
CC PTM: PHOSPHORYLATED AT SER/THR RESIDUES.  
CC [3]  
CC SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.  
CC [4]  
CC SIMILARITY: CONTAINS 2 FIBRINOGEN-LIKE TYPE III-LIKE DOMAINS.  
CC [5]  
CC SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.  
CC [6]  
CC DATABASE: NAME=PRO; NOTE=CD guide CDw119 entry;  
CC WWW="http://www.ncbi.nlm.nih.gov/ncbi/cd/cdw119.htm".  
CC [7]  
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CC -----  
DR EMBL: J03143; AAA52731.1; -  
DR PIR: A31555; A31555.  
DR PDB: 1JRH: 25-MAR-98.  
DR PDB: 1FC9: 11-AUG-00.  
DR GlycositeDB: P15260; -  
DR MIM: 107470; -  
DR MIM: 209950; -  
KW Receptor; Transmembrane; Glycoprotein; Signal; Phosphorylation;  
KW Immunoglobulin domain; 3D-structure.  
FT SIGNAL 1 17  
FT CHAIN 18 489 INTERFERON-GAMMA RECEPTOR ALPHA CHAIN.  
FT DOMAIN 18 245 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 246 266 POTENTIAL.  
FT DOMAIN 267 489 CYTOPLASMIC (POTENTIAL).  
FT DISULFID 77 85  
FT DISULFID 122 167  
FT DISULFID 195 200  
FT DISULFID 214 235  
FT CARBOHYD 34 34 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 79 79 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 86 86 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 179 179 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 240 240 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 489 AA; 54404 MW; DCF9E574DBF47400 CRC64;  
Query Match 7.4%; Score 121; DB 1; Length 489;  
Best Local Similarity 21.6%; Pred. No. 0.0022;  
Matches 61; Conservative 54; Mismatches 10; Indels 66; Gaps 13;  
QY 35 LPAPONLSVLSTNMKHLMSVPIAGETVY-----YSEYGEYESLYTSHWIPSSW 88  
DB 29 VPTPTNVITTESNMNPVYMEYQIMPQVFEVKNKGVK-----NSEMIDA-- 76  
QY 89 CSLTGPCEVDYTDITAVPYN---LRYRATGSGTSSAMSLKHPNRRSTLTTPGMEI 145  
DB 77 GINSHHYCNISDHVGD--PSNSLWRYVAVRQKESAYAKSEEPVACRDGIGPKLDI 134  
QY 146 KXGPHLYTEL-----EDLGPQFE-FLVAY--WKEPQAEHYVMVNSG--- 186  
DB 135 RKEKQIMIDIFHPSPVFNAGDEVDYDEPTTCYIRVNVYRAMGSELYQYKILQKEND 194  
QY 187 -----GIPVHLETMERGAAYCYKAGTFVRAIGYSAFSQTECEYVGEA-----IP 232  
DB 195 CDEIQCOLAIPV-----SSLSQYCVASAEGLVHMVGVTTEKSKREVCITFNSSIKSLMIP 250  
QY 233 LVLAFAVGFMLLVVVPFLFVWKMGRLLQYSCPPVVPDIL 275  
DB 251 VVAALLFL--VLSLVFCFYIKINPLKEKS---IILPKSL 287  
RESULT 14  
TF\_MOUSE STANDARD; PRT; 294 AA.  
AC P20352;  
DT 01-FEB-1991 (Rel. 17, Created)  
DT 01-AUG-1991 (Rel. 19, Last sequence update)  
DT 01-OCT-2000 (Rel. 40, Last annotation update)  
DE TISSUE FACTOR PRECURSOR (TF) (COAGULATION FACTOR III).  
GN F3 OR CF3 OR CF-3.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RN SEQUENCE FROM N.A.  
RP MEDLINE=91093171; PubMed=1985911;  
RT Ranganathan G., Blatti S.P., Subramaniam M., Fass D.N., Mahle N.J.,  
RA Getz M.J.;  
RT "Cloning of murine tissue factor and regulation of gene expression by  
transforming growth factor type beta 1.";



RL J. Biol. Chem. 266:496-501(1991).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BALB/C;  
 RX MEDLINE=89343974; PubMed=2761539;  
 RA Hartzell S., Ryder K., Iannan A., Iau L.F., Mathans D.;  
 RT "A growth factor-responsive gene of murine BALB/c 3T3 cells encodes a  
 RL protein homologous to human tissue factor".  
 RL Mol. Cell. Biol. 9:2567-2573(1989).  
 CC -1- FUNCTION: INITIATES BLOOD COAGULATION BY FORMING A COMPLEX WITH  
 CC CIRCULATING FACTOR VII OR VIIA. THE [TF-VIIA] COMPLEX ACTIVATES  
 CC NORMAL HEMOSTASIS BY INITIATING THE CELL-SURFACE ASSEMBLY AND  
 CC PROPAGATION OF THE COAGULATION PROTEASE CASCADE.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- SIMILARITY: BELONGS TO THE TISSUE FACTOR FAMILY.  
 CC  
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 CC  
 CC EMBL; M57896; AAA63400.1; -  
 CC DR EMBL; M26071; AAA64014.1; -  
 CC DR PIR; A32318; KFM53.  
 CC DR HSSP; P13726; ITRH.  
 CC DR MGD; MGI:88381; F3.  
 CC DR InterPro; IPR001187; -  
 CC DR Pfam; PF01108; Tissue\_fac; 1.  
 CC DR PRINTS; PR00346; TISSUEFACTOR.  
 CC DR PROSITE; PS00621; TISSUE\_FACTOR; 1.  
 CC Glycoprotein; Blood coagulation; Transmembrane; Signal; Lipoprotein;  
 CC Palmitate.  
 CC FT CHAIN 1 28  
 CC FT SIGNAL 1 28  
 CC FT CHAIN 29 294  
 CC FT DOMAIN 29 251  
 CC FT TRANSMEM 252 274  
 CC FT DOMAIN 275 294  
 CC FT SITE 245 247  
 CC FT CARBOHYD 37 37  
 CC FT CARBOHYD 57 57  
 CC FT CARBOHYD 169 169  
 CC FT CARBOHYD 200 200  
 CC FT DISULFID 75 83  
 CC FT DISULFID 218 241  
 CC FT LIPID 215 275  
 CC CONFLICT 26 26  
 CC SEQUENCE 294 AA; 32935 MW; A306101293C31FA0 CRC64;

Query Match 7.3%; Score 119.5; DB 1; Length 294;  
 Best Local Similarity 23.3%; Pred. No. 0.0017;  
 Matches 74; Conservative 39; Mismatches 115; Indels 89; Gaps 17;

QY 22 ALIP-----CLTDEVALIPAPD---NLSTLSTNMKHLMSVYAPGETVY-YSEVYQGE 73  
 DB 12 ALAPFLCLCLQVYAGAGIPEKAFNLWISTDFKTIEMQ---PKPTNYTYTVOISDR 67  
 QY 74 YESLTSHTWIPSSWCSLTREPCEDVTDIT--ATVPYNLARATL-----SQ----- 120  
 DB 68 -----SRNW--KNKCESTTDECDLTDEIVKDVWYAEAKLVSPRRNSVHGQDQVLI 119  
 QY 121 -----TSAMSLKHPNRSNLTILRPGME-----IKKXGFHLVI 154  
 DB 120 HGEPPFTNAPKFLPY-----RDTNIGQPIYIQFEDGRKLNVVVVDLSLTVKKNGFLL 175  
 QY 155 ELEDIGPQFEFLVAV--WMREPGAEHVAKVNRSGIIPVHLETPGAAVC--VKAQTFVKA 211  
 DB 176 R-QVGGKDLGYITTYRKSSSTGKNTINTNTNFSIDV-----EEGVSYCVFQVAMIFSRK 229

QY 212 IGYSAFSQTECYE----VOGEAIPVLALFAFVGMILLIVVPLVWKNGLQYSCCP 267  
 DB 230 TNONSGSSSTVCYCEQWKSFGELITIVGANVLLATITFIILSLCKRRNRAGQ----- 284  
 QY 268 VVVLPTLKITNSPKL 284  
 DB 285 -----KGNKTPSRLL 293

RESULT 15  
 TF\_BOVIN  
 ID TF\_BOVIN STANDARD; PRT; 292 AA.  
 AC P30931;  
 DT 01-JUL-1993 (Rel. 26, created)  
 DT 01-JUL-1993 (Rel. 26, last sequence update)  
 DT 01-OCT-2000 (Rel. 40, last annotation update)  
 DE TISSUE FACTOR PRECURSOR (TF) (COAGULATION FACTOR III).  
 GN F3.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
 RC TISSUE-Adrenal gland;  
 RX MEDLINE=92109720; PubMed=1764065;  
 RA Takayanoki Y., Muta T., Miyata T., Iwanaga S.;  
 RT Biochem. Biophys. Res. Commun. 181:1145-1150(1991).  
 CC -1- FUNCTION: INITIATES BLOOD COAGULATION BY FORMING A COMPLEX WITH  
 CC CIRCULATING FACTOR VII OR VIIA. THE [TF-VIIA] COMPLEX ACTIVATES  
 CC FACTORS IX OR X BY SPECIFIC LIMITED PROTOLYSIS. TF PLAYS A ROLE IN  
 CC NORMAL HEMOSTASIS BY INITIATING THE CELL-SURFACE ASSEMBLY AND  
 CC PROPAGATION OF THE COAGULATION PROTEASE CASCADE.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- SIMILARITY: BELONGS TO THE TISSUE FACTOR FAMILY.  
 CC  
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 CC  
 CC EMBL; S74147; AAB20755.1; -  
 CC DR PIR; JQ1319; KEB03.  
 CC DR HSSP; P24055; IAZ1.  
 CC DR InterPro; IPR001187; -  
 CC DR Pfam; PR001108; Tissue\_fac; 1.  
 CC DR PRINTS; PR00346; TISSUEFACTOR.  
 CC DR PROSITE; PS00621; TISSUE\_FACTOR; 1.  
 CC Glycoprotein; Blood coagulation; Transmembrane; Signal; Lipoprotein;  
 CC Palmitate.  
 CC FT SIGNAL 1 35  
 CC FT CHAIN 36 292  
 CC FT DOMAIN 36 248  
 CC FT TRANSMEM 249 271  
 CC FT DOMAIN 272 292  
 CC FT SITE 46 48  
 CC FT CARBOHYD 43 43  
 CC FT CARBOHYD 153 153  
 CC FT CARBOHYD 181 181  
 CC FT DISULFID 81 89  
 CC FT DISULFID 215 238  
 CC FT LIPID 274 274  
 CC SEQUENCE 292 AA; 32475 MW; 5E471092BFBCE163 CRC64;

Query Match 7.0%; Score 114.5; DB 1; Length 292;  
 Best Local Similarity 19.8%; Pred. No. 0.0046;  
 Matches 49; Conservative 39; Mismatches 103; Indels 57; Gaps 9;

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QY 40 NLSVLTNNKHLMMSPVIAPEGTVYYSVEYQGEYESLTSHT-----WIPSSMCSLFE 93
Db 43 NITWKTNEFKTILEMEP-----KPINHYTVQISPRLGW--KNKCFYTT 85
QY 94 GPECDDYDDITATVAPYMLRVARATLGSQTSAMSILKHPENRN-----STILTRPGE-I 145
Db 86 NTECDYTDYKKNVRETYLARVLSTYPADTSSSTVEPPPTNSPEFTPILETNLGQPTIOSF 145
QY 146 KXKGFLVIELED-----LGPOFEFLVAYXREPGEAEHVKMVRSGI 188
Db 146 EOYGTKLNTVYQDARTLVBRANSAPLSLNDYVGKDLNTLYYWKASSTGKKKATNTNG-- 203
QY 189 PVHLEMEPGAAYCVKAQTV--KAIGXYSASFQTECVVOGEAIPVLAIPAFVGEMLI 246
Db 204 --FLIDVDKGENYCFHVOAVILSRVNOKSPESPIKCTSHEK---VLSTELFLIGTYML 258
QY 247 LVVVPFLV 254
Db 259 VIIIFIVV 266

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Job time: 112 sec